STIC-Biotech/ChemLib

153748

From:

Hutzell, Paula

Sent:

Wednesday, May 18, 2005 7:07 AM Graser, Jennifer; STIC-Biotech/ChemLib

To: Subject:

RE: rush search

approved

-----Original Message-----

From:

Graser, Jennifer

Sent:

Tuesday, May 17, 2005 4:48 PM

To: Subject: Hutzell, Paula rush search

Importance: High

Hi Paula,

Could you please authorize this rearch for an amendment which is due?

Thanks, Jennifer

STIC:

Please search SEQ ID NO: 1 and 2 for Serial No. 10/650,123 in pending and commercial

databases.

Thanks,

Jennifer Graser

REM 3B09 (mailbox 3C18)

Art Unit 1645

272-0858

Interference Search in Exisoffice

STAFF USE ONLY

Searcher: ______ Searcher Phone: 2-Date Searcher Picked up: _____ Date Completed: _____ Searcher Prep/Rev. Time: ____ Online Time: ____

NA#:____ AA#:__ Interference:___ SPDI:__ S/L:___ Oligomer:___ Encode/Transl:___

Structure#:_____ Text: Inventor:____ Litigation:___ **********************
Vendors and cost where applicable STN:______

LEXIS/NEXIS:______SEQUENCE SYSTEM:_____ WWW/Internet:_____

Other(Specify):_

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AX685933 Sequence
AR167417 Sequence
AR167420 Sequence
US2067 Neisseria m
AR167415 Sequence
CQ014510 Sequence
CQ771466 Sequence
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AF175680 525 bp DNA linear BCT 06-SEP-1999
Neisseria meningitidis strain M986 surface protein A (nspA) gene,
complete cds.
AF175680
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VRSGELSVGVRVKF"
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1 (bases 1 to 525)

8 Moe,G.R., Tan,S. and Granoff,D.M.
Differences in Surface Expression of Neisserial Surface Protein, among Neisseria meningitidis Group B strains
L. Infect. Immun. (1999) In press
2 (bases 1 to 525)
2 Moe,G.R., Tan,S. and Granoff,D.M.
Direct Submission
L. Submitted (04-AVG-1999) Children's Hospital Oakland Research
Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA
Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA
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Organism="Neisseria meningitidis"
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CQ84512 Sequence
U52066 Neisseria
AR15578 Neisseria
AE002420 Neisseria
AE07416 Sequence
AE175678 Neisseria
AF175677 Neisseria
AF175676 Neisseria
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AF175682 Neisseria
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Neisseria meningitidis strain NGP165 surface protein A (nspA) gene,
complete cds.
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100.0%; Score 525; DB 1;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 525; Conservative 0; Mismatches 0;
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Moe,G.R., Tan,S. and Granoff,D.M.

Differences in Surface Expression of Neisserial Surface Protein Jamong Neisseria meningitidis Group B strains

2 (bases I mmun. (1999) In press

2 (bases I Tan,S. and Granoff,D.M.

Direct Submission
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Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA
Location/Qualifiers
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100.0%; Score 525; DB 1;
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   Betaproteobacteria; Neisseriales;
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                                                                                                                                                                            /organism="Neisseria meningitidis"
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                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 525; DB 6; Best Local Similarity 100.0%; Pred. No. 1.5e-96; Matches 525; Conservative 0; Mismatches 0;
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CQ814512.1 GI:47603711
Bacteria; Proteobacteria;
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                                                       Martin, D. and Rioux, S.
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VRSGELSVGYRVKF
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 Submitted (04-AUG-1999) Children's Hospital Oakland Research
Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA
Location/Qualifiers
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                                                       1. .525
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'gene="nspA"
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/translation="wkkalmtlalalpaalaegasgfyvqadaahakassslgsak
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VRSGLSVGVRVKF"
143. 1199
                                                                                                                                                                                                                                          Submitted (22-MAR-1996) Denis Martin, Department of Microbiology, University Laval, Unite de Vaccinologie, Laboratoire et Service d'Infectiologie, Centre Mospitalier de l'Universite Laval, 2705 boul Laurier, Ste-Foy, Quebec GIV 4G2, Canada
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                                                                        Bactericidal and cross-protective activities of a monoclonal antibody directed against Neisseria meningitidis NspA outer membrane protein
                       3 (bases 1 to 830)
Cadieux, N., Plante, M., Rioux, C.R., Hamel, J., Brodeur, B.R.
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100.0%; Pred. No. 1.5e-96;
iive 0; Mismatches 0;
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Best Local Similarity 100.
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GlaxoSmithKline Biologicals S.A. (BE); Utrecht University (NL) Location/Qualifiers
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Plante,M., Cadieux,N., Rioux,C.R., Hamel,J., Brodeur,B.R. and
Martin,D.
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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1 (bases 1 to 830)
Martin, D., Cadieux, N., Hamel, J. and Brodeur, B.R.
Highly conserved Neisseria meningitidis surface protein protection against experimental infection
J. Exp. Med. 185 (7), 1173-1183 (1997)
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                                                                                                                                                     Length 525;
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810 bp DNA linear
Neisseria meningitidis outer membrane protein gene,
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                                    1. .525
Organism="Neisseria meningitidis"
/mol_type="unassigned DNA"
/db_xref="taxon:487"
                                                                                                                                                 Query Match
100.0%; Score 525; DB 6;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 525; Conservative 0; Mismatches 0;
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Neisseriaceae, Neisseria.

S. Moo.G.R., Tan.S. and Granoff, D.M.
Differences in Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains
L. Infect. Immun. (1999) In press
E. Z. (bases 1 to 525)
S. Moo.G.R., Tan.S. and Granoff, D.M.
Direct Submission
L. Submitted (04-MUG-1999) Children's Hospital Oakland Research Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA
Location/Qualifiers
I. 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /trānslation="MKKALATLIALADPAAALAEGASGFYVQADAAHAKASSSLGSAK
GREPRISAGYRINDLRFAVDYTRYKKYKAPSTDFKLYSIGAGAIYDPDYGSPVKFYLG
ARLSLARASVDLGGSDSFSQTSIGLGVLTGVSXAVTPNVDLDAGYRYNYIKI
VRSGBLSAGYRVKF.
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/mol_type="genomic DNA"
/strain="CU385"
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/transi table=11
/product="surface protein A"
/protein id="AAD53281.1"
/db_xref="G1:5825531"
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                                                     Neisseria meningitidis
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Brodeury, B.R., Martin, D., Hamel, J. and Rioux, C.
Proteinase K resistant surface protein of neisseria meningitidis
Patent: US 6287574-A 1 11-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCGATTTGGATGCCGGCTACCGCTACATACATCGGCAAAGTCAACACACTGTCAAAAAC
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                                                         623 GTCCGTTCCGGCGACTGTCCGTCGGCGTGCGCGTCAAATTCTGA
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                                    GTCCGTTCCGGCGAACTGTCCGTCGGCGTGCGCGTCAAATTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 525; DB 6;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 525; Conservative 0; Mismatches 0;
                                                                                                                                                                   DNA
                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="unknown"
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Sequence 1 from patent US 6287574.
                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                      AR167414.1 GI:17903193
                                                                                                                                                                                                                                                                                                                                                                                                             1. .830
                                                                                                                                                                                                                                                                                               Unclassified.
                                                                                                                                                                                                                                                         Unknown.
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DRGNSMET INGVAAGALNP I SAGEAVDOMYGENPAAETVEALVNYLPFAKYKNLT
KAARDGKAAVGGDFSDS YKHNTASRLSQS VDGEMFQTRNVDFKAKS I GTKI HDGAQGK
HISGHRINY I EGKSTLINQUI NPQELLINGI HSGAYPVI SKGARGNPVVDFGYPI GSDGKS
GLSTNFGT I HSGKNGVHI V PANPKTI KKVQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to GP:4838554 percent identity: 79.35; identified by sequence similarity; putative" (codon start=1 (rans]_teble=11
                                                                                                                                                                                                                           343. .1232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MafB-related protein; identified by Oxford;
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1355. .2296
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/gene="NMB0653"
2300. .3568
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/gene="NMB0654"
3571. 2000
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843. .1232
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/gene="NMB0654"
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S Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C.,
Tettelin, H., Saunders, N.J., Ketchum, K.A., Hood, D.W., Peden, J.F.,
Dodson, K.E., Eisen, J.A., Ketchum, K.L., DeBoy, R., Peterson, J.D.,
Hickey, E. K., Haft, D.H., Salzberg, S.L., White, O., Fleischmann, R.D.,
Dougherty, B.A., Mason, T., Ciecko, A., Parksey, D.S., Blair, E.,
Cittone, H., Clark, E.B., Cocton, M.D., Utterback, T.R., Khouri, H.,
Qin, H., Vamathevan, J., Gill, J., Scarlato, V., Masignani, V.,
Pizza, M., Grandi, G., Sun, L., Smith, H.O., Fraser, C.M., Moxon, E.R.,
Rappuoli, R. and Venter, J.C.
Direct Submission
L Submitted (17-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                             Neissaca
Neisseria meningtidis serogroup B strain MC58 section 62 of 206 of
the complete genome.
AE002420 AE002098
AE002420.1 GI:7225876
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HQDTGRMQLIREGLHHDTGHIGWEAMNKGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseriaceae; Neisseria.

1 (bases 1 to 10057)

Tettelin,H., Saunders,N.J., Heidelberg,J., Jeffries,A.C.,
Nelson,K.E., Elsen,J.A., Ketchum,K.A., Hood,D.W., Peden,J.F.,
Nodson,R.J., Nelson,W.C., Gwinn,M.L., DeBoy,R., Peterson,J.D.,
Hickey,E.K., Haft,D.H., Salzberg,S.L., White,O., Fleischmann,R.D.,
Dougherty,B.A., Mason,T., Ciecko,A., Parksey,D.S., Blair,E.,
Cittone,H., Clark,E.B., Cotton,M.D., Utterback,T.R., Khouri,H.,
Qin,H., Vamathevn,J., Gill,J., Scarlato,V., Masignani,V.,
Pizza,M., Grandi,G., Sun,L., Smith,H.O., Fraser,C.M., Moxon,E.R.,
Rappuoli,R. and Venter,J.C.
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Neisseria meningitidis MC58
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
     GTCCGTTCCGGCGAACTGTCCGTCGGCGTCCGAATTCTGA 525
                            481 GTCCGTTCCGGCGAACTGTCCGCCGGTGTGCGCGCTCAATTCTGA 525
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90786 AIGAAAAAAGCACTIGCCACACTGATIGCCCTCGCTCTCCCGGCCGCCGCACTGGCGGAA 90727
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                                                                                                                                        TTCGCCGTCGATTACACGCGCTACAAAACTATAAAGCCCCATCCACCGATTTCAAACTT
                                                                                                                                                                                                                    TACAGCATCGGCGTCCGCCATTTACGACTTCGACACCCAATCGCCCGTCAAACCGTAT
                                       GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC
                                                          GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC
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Neisseria meningitidis
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Neisseriaceae, Neisseria.
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YCYYIEISDGIGNNQTLISNKIHPPYSQGKNIQAGELKKGDTLLSESGAKGTVQNITF
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KSRAPTNGQAALDNSVQYKSTSPRRVGYDKANNEIVVLNKTQTFNNGSAEYHGHVRSW
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LSKNKDLDIAGLSLTCFGHLARLHSNIGDYDKVIPLLHSKQDDPELQGRAEDALEDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MLLPRQHLGONGRRLKSKHRPSCCRLRMSTGOPQCRRNRRSRLQ
HCRRQSRKVGKNGKTGEIKADGRKVNVRIDSTEADLLYPAGQ"
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MPPKPSKPPSTLPPPKPQSWQKR"
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                                       'note="hypothetical protein; identified by Glimmer2;
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/protein_id="AAF62315.1"
/db_xref="G1:7413437"
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protein_id="AAF41077.1"
db_xref="G1:7225884"
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protein_id="AAF41075.1"
db_xref="G1:7225882"
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product="hypothetical pi
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'db_xref="G1:7225883"
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/codon_start=1
/transl_table=11
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/translation="MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAK
GFSPRISAGYRINDLRFAVDYTRYKNYKABGTDFKLYSIGASAIYDFDTQSPVKPYLG
ARLSLNRASVDLGGSDSFSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKN
VRSGRASAGVKVKF"
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Brodeur, B.R., Martin, D., Hamel, J. and Rioux, C.
Proteinase K resistant surface protein of neisseria meningitidis
Patent: US 6287574-A 5 11-SEP-2001;
Location/Qualifiers
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Pred. No. 3e-95;
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Pred. No. 3e-95;
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AR167416.1 GI:17903195
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   GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACAAAAGCCTCAAGCTCTTTA 90667
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Neisseria meningitidis outer membrane protein gene, complete cds.
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Submitted (22-MAR-1996) Denis Martin, Department of Microbiology
Submitted (22-MAR-1996) Denis Martin, Department of Microbiology
University Laval, Unite de Vaccinologie, Laboratoire et Service
d'Infectiologie, Centre Hospitalier de l'Universite Laval, 2705
boul Laurier, Ste-Foy, Quebec GlV 4G2, Canada
Location/Qualifiers
                                                                                                                          90546 TACAGCATCGCCGCTCCGCCATTTACGACTTCGACACCCAATCGCCCGTCAAACCGTAT
                                                                                                                                                                                                                                                                      90486 CTCGGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACTTGGGCGCAGCGACGACTTC
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                                                                                                                                                                              TACAGCATCGGCGCGTCCGCCATTTACGACTTCGACACCCCAATCGCCCGTCAAACCGTAT
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                                                                       GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC
                                                                                                          TTCGCCGTCGATTACACGCGCTACAAAACTATAAAGCCCCCATCCACCGATTTCAAACTT
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Neisseria meningitidis
Bacteria, Froteobacteria, Betaproteobacteria, Neisseriales,
Neisseriaceae; Neisseria.
1 (bases 1 to 850)
Cadieux,N., Plante,M., Rioux,C.R., Hamel,J., Brodeur,B.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody directed against Neisseria meningitidis NspA outer membrane protein Infect. Immun. 67 (9), 4955-4959 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Neisseria meningitidis"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208. .732
/codon start=1
/transl_table=11
/product="outer membrane protein"
/protein id="AAB41580.1"
/db_xref="G1:1808967"
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/clone="pNP2205"
140. .145
196. .199
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/Gene="NOAD700"

Complement (1101. 2327)
/gene="NOAD700"

Complement (1101. 2327)
/gene="NOAD700"

/note="NOAD700"

similar to SW.RBN_ECOLI (EMBL:L19201), rbn, Escherichia similar to SW.RBN_ECOLI (EMBL:L19201), rbn, Escherichia coli ribonuclease BN (EC 3.1.-.-), fasta scores; E(): 2.3a-28, 34.3% identity in 268 as overlap. Longer than rbn at the C-terminus. Also similar to TR:08549

(EMBL:AF067083) Vitreoscilla sp. hypothetical protein (376 as), fasta scores; E(): 0, 45.0% identity in 333 as overlap. Contains a scores; E(): 0, 45.0% identity in 45 as overlap. Contains a hydrophobic, possible membrane-spanning regions,
                                                                                                                                                                                                                                                                                                                                                                                         /product="putative periplasmic protein"
/protein_id="CAB83985.1"
/db_xref="G1:7379425"
/db_xref="Uniprot/TrEMBL:09JQQ2"
/tb_nslation="MJTKLKILPFPFPVJAINLLFFFFSSDIESFGNYOFEYVYD
KGWPANYILWKDGNEGNFDKIISGLVLEYYKEDDNIYFSYIDGGGFASDSCYYKPEI
LYGKIILNKNHIININSMEKNNFLSEDKIMKGTRNWLADPKNKCNIQTLD"
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VGSVODAALASGAPOWSGALRTAATLTFWTLLIWGLYRFVPNRFVPARQAFVGALATA
PCLETARSLEFWYMGNFDGYRSIYGAFAAVPFFLLWIALLWTLVLGGAVLTSSLSYWO
GEAFRRGFROFTRAYLILLLDAAQKEGKALPVOEFRRHINMGYDELGELLEKLA
RHGYIYSGROGWVLKTGADSIELNELFKLFVYRPLPVERDHVNQAVDAVMMPCLGTLN
MTLAEFDAQAKKQOGS"
                                                                                                                                                                                                                                                    /note="NWA0698, possible periplasmic protein, len: 152 aa, unknown, contains a probable N-terminal signal sequence and lies within a region of unusually low GC content"
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ALVPVLTVMVAVASIFPVFDRWSDSFVSFVNQTIVPQGADMVFDYINAFREQANRLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ^codon_start=1
/transl_table=11
/product="putative_ABC transporter protein (pseudogene)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="NMA0699"
/force="NMA0689"
/note="NMA0689, pseudogene, probable ABC transporter
protein, len: 336 bp; similar to C-termini of many ABC
transporters e.g. TR:Q46973 (EMBL:U47048), mtfB,
Escherichia coli microcin transport protein (707 aa),
fasta scores; E(): 2.6e-19, 53.2% identity in 111 aa
overlap. Contains PS00211 ABC transporters family
signature. NMA0686 may be the remainder of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   868. .912 '
/gene="NNA0699"
/note="PS00211 ABC transporters family signature"
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/transl_table=11
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/protein_id="CAB83987.1"
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/db_xref="GOA:Q9JVT9"
/db_xref="Uniprot/TrEMBL:Q9JVT9"
     /mol_type="genomic DNA"
/strain="Z2491"
                                                        /db_xref="taxon:122587"
/note="serogroup: A"
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/gene="NMA0698"
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/gene="NMA0699"
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/transl_table=
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/pseudo
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GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA 327
                                                                                                                                                                                                  GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC 180
                                                                                                                                                                                                                                        328 GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC 387
                                                                                                                                                                                                                                                                                                                                                           388 TICGCCGICGATIACACGCGCTACAAAACTAIAAAGCCCCAICCACCGATIICAAACTI 447
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Neisseria meningitidis serogroup A strain Z2491 complete genome;
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1 (bases 1 to 31321)
Parkhill, J. Achtman, M., James, K.D., Bentley, S.D., Churcher, C., Ries, S.R., Morelli, G., Basham, D., Brown, D., Chillingworth, T., Davies, R.M., Davis, P., Deviln, K., Feltwell, T., Hamlin, N., Holroyd, S., Jagels, K., Leather, S., Moule, S., Mungall, K., Quail, M.A., Rajandream, M.A., Rutherford, K.M., Simmonds, M., Skelton, J., Whitehead, S., Spratt, B.G. and Barrell, B.G. Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22391
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(URL, http://www.sanger.ac.uk/Projects/N_meningitidis/).

Location/Qualifiers
1. 311321
                                                                                                                                                                                                                                                                                                                  TTCGCCGTCGATTACACGCGCTACAAAACTATAAAGCCCCCATCCACCGATTTCAAACTT
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Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
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Neisseria meningitidis 22491
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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AL162754 AL157959
AL162754.2 GI:7379424
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149677 TTGGCGGTCGATTACACGCGCTACAAAACTATAAAGCCCCATCCACGGATTTCAAACTT 149618
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DADKIHIDGWQVVEWADGYDIAVSETPKTKMPSENAPRLYFANVGGYRAGQLAEAHAF
GLFAAATPAEAKQKALQTLLTDSYVQQHKDNLKDVDNLLALDRIGNFHIRLTPNPHGK
PAEIGFQGYLPI"
                                                                                                                                                                                                                                                                                                                             /note="NWA0704, len: 140 aa; similar to many hypothetical proteins e.g. SW:YB90 HAEIN (EMBL:102798), H11190, Haemophilus influenze hypothetical protein (141 aa), fasta scores; E(): 5.1e-32, 58.0% identity in 138 aa overlap. Shows very weak similarity to eukaryotic (EMPL:M77850), pts, Rattus norvegicus 6-pyruvoyl pts, Rattus norvegicus 6-pyruvoyl pts, Rattus norvegicus 6-pyruvoyl tetrahydrobiopterin synthase precursor (EC 4.6.1.10) (144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCGATTTGGATGCCGGCTACCGCTACAACTACATCGGCAAAGTCAACACTGTCAAAAAC 480
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Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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                                                                                   3782. 3791
/gene="NMA0703"
/note="Core DNA uptake sequence: gccgtctgaa"
/label=DUS
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Pred. No. 2.1e-95;
0; Mismatches 4
                                                                                                                                                                                                   4083. .4505
/gene="NMA0704"
4083. .4505
/gene="NMA0704"
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complete cds.
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/protein id="CAB83990.1"
/bc.xref==[G1:7379429]
/db.xref=="Uniprot/TrEMBL:09JVT7"
/translation="MPKLHMFYLGGNAGRSNIEVHDIQFAVCDDYREAVPALKAAWFG
                                                                                                                                                                                                                                                                                                                                                                                 Mote-"MMA0701, possible pseudogene, len: 258 bp; shows weak similarity to part of SW:WRBA_ECOLI (EMBL:M99166), wrbA, Escherichia coli Trp repressor binding protein (197 aa), fasta scores; E(): 0.064, 29.3% identity in 82 aa coverlap. Also similar to part of TR:085450 (EMBL:AF067083) Vitreoscilla sp. Trp repressor binding protein (fragment) (124 aa), fasta scores; E(): 6.6e-14, 56.6% identity in 83
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VELBRARMAQDIGVKQTYLDLSLMRQTTHNALMDDTAAIFTABNGYPWFFVDGRNAL
FLLYAAIYAKGQDIRHIIAGVETDFSGYPDCRDYFVKSMNYTLNLAMDYDFQIHTPL
MYLTKAQTWALADEMGALDYIREQTHTCYNGIVGGCRECPSCILRERGLAEYLBSKKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="hypothetical protein NMA0701 (pseudogene)"
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/label=DUS
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/note="Core DNA uptake sequence: gccgtctgaa"
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/note="Core DNA uptake sequence: gccgtctgaa"
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/note="Core DNA uptake sequence: gccgtctgaa"
   note="Core DNA uptake sequence: gccgtctgaa"
                                                                                          gccgtctgaa"
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                                                                                       'note="Core DNA uptake sequence:
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/db_xref="UniProt/TrEMBL:Q9JVT8"
                                                           .2426)
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/gene="NMA0701"
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/gene="NMA0701"
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/transl_table=
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/pseudo
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1 (bases 1 to 525)
Moe,G.R., Tan,S. and Granoff,D.M.
Moe,G.R., Tan,S. and Granoff,D.M.
Differences in Surface Expression of Neisserial Surface Protein & among Neisseria meningitidis Group B strains
Infect. Immun. (1999) In press
2 (bases 1 to 525)
Moe,G.R., Tan,S. and Granoff,D.M.
Direct Submission
Submitted (04-AUG-1999) Children's Hospital Oakland Research Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA
Institute, Advoice Protein Protein
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Moe,G.R., Tan,S. and Granoff,D.M.
Direct Submission
Submitted (04-AUG-1999) Children's Hospital Oakland Research
Institute, 747 Pifty-Second Street, Oakland, CA 94609, USA
Location/Qualifiers Neisseria meningitidis Neisseria meningitidis Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; ö ch 98.5%; Score 517; DB 1; Length 525; Stanilarity 99.0%; Pred. No. 6.5e-95; Conservative 0; Mismatches 5; Indels strains 1. .525 /organism="Neisseria meningitidis" Neisseriaceae, Neisseria.

1 (baees 1 to 525)

Moe,Gr., Tan, S. and Granoff,D.M.

among Neisseria meningitidis Group B

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GenCore version 5.1.6
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nucleic search, using sw model OM nucleic

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Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

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47	9.0	1842	۵	ADA71243	Ada71243 Rice gene
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ALIGNMENTS

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Neisserial surface protein A; NspA; refolding; recombinant production; vaccine; subunit vaccine; prevention; diagnosis; meningococcus; invasive bacterial disease; bacteraemia; meningitis; Neisseria gonorrhoeae; gonorrhoeae; mature protein; strain H44/76; antibacterial; gene therapy; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                        Poolman J;
                                                                                                                                                                                                                                                                                                                                                                                                        Goraj K,
                                                                                                                                                                                                      /*teg= b
/product= "NspA"
1..57
4.tag= a
58..522
/*tag= c
/product= "Mature NspA"
                                                                              Neisseria meningitidis H44/76 NspA gene.
                                                                                                                                                                                                                                                                                                                                                                                                        Feron C,
                                                                                                                                                                                                                                                                                                                                                                       (GLAX ) GLAXOSMITHKLINE BIOLOGICALS SA (UYUT-) RIJKSUNIV UTRECHT.
                                                                                                                                                                             Location/Qualifiers
1. .525
                                                                                                                                                               Neisseria meningitidis; H44/76.
                   BP
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Tommassen J, Weynants V;
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                                                                                                                                                                                                                                                                                                                                 28-AUG-2003; 2003WO-EP010085
                   ADL13427 standard; DNA; 525
                                                            (first entry)
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                                                            03-JUN-2004
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                                       ADL13427;
RESULT 1
          ADL13427
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Disclosure; Fig 3; 62pp; English P-PSDB; ADL13428,

Sequence 525 BP; 117 A; 186 C; 119 G; 103 T; 0 U; 0 Other;

360 GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACAAAAGCCTCAAGGTCTTTA 120 120 GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC 180 TICGCCGTCGATTACACGCGCTACAAAACTATAAAGCCCCATCCACCGATTTCAAACTT 240 181 Trogcogrocartacacococracaaaacraraaaccccarccaccoartroaaacrr 240 TACAGCATCGCCGCCGTTTTACGACTTCGACACCCCAATCGCCCGTCAAACCGTAT 300 241 TACAGCATCGGCGCGTCCGCCATTTACGACTTCGACACCCAATCGCCCGTCAAACCGTAT 300 CTCGGCGCGCGCTTGAGCCTCAACCGCGCTCGTCGACTTGGGCGGCAGCGACAGCTTC 360 AGCCAAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAAGCTATGCCGTTACCCCGAAT 420 GTCGATTTGGATGCCGGCTACCGCTACACTACATCGGCAAAGTCAACACTGTCAAAAAC 480 9 9 1 ATGAAAAAGCACTTGCCACACTGATTGCCCTCGCTCTCCCGGCCGCCGCGCTTGGCGGAA 61 GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA CTCGGCGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACTTGGGCGGCAGCGACAGCTTC Gaps ; 0 100.0%; Score 525; DB 12; Length 525; 100.0%; Pred. No. 4.7e-125; 0; Indels 0; Mismatches Matches 525; Conservative Local Similarity 301 241 361 61 121 181 361 421 421 Query Match 301 ð g g ò g 셤 g ò g

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ds; gene; NspA; vaccine; antibacterial; meningitis. 100.0%; Score 525; DB 12; 100.0%; Pred. No. 4.7e-125; ive 0; Mismatches 0; meningitidis strain 608B NspA coding sequence. Location/Qualifiers 1. .525 /*tag= a /product= "NspA" Claim 9; Fig 1; 79pp; English. 29-AUG-2003; 2003WO-CA001452. 30-AUG-2002; 2002US-0406980P. ADL24351 standard; DNA; 525 (first entry) 608B NspA coding sequence. (SHIR-) SHIRE BIOCHEM INC. Best Local Similarity 100. Matches 525; Conservative Neisseria meningitidis WPI; 2004-239123/22. P-PSDB; ADL24352. Martin D, Rioux S; WO2004019976-A2. meningitidis. 03-JUN-2004 11-MAR-2004. ADL24351; 7 61 61 Query Match RESULT ADL243 셤 ઠે Š 셤 ò 셤 The invention relates to an isolated refolded Neisserial surface protein

A (NspA) from Neisseria meningitidis or Neisseria gonorrhoeae. The
invention also relates to the method of refolding an NspA protein; an
alkaline refolding buffer comprising ethanolamine and SB-12 (3dimethyldodecylammoniopropanesulphonate) for refolded NspA protein; a
pharmaceutical composition comprising the refolded NspA protein; a
carrier and optionally one or more other Neisserial antigens; a method of
preventing or treating a Neisserial infection; NspA has
corrier the NspA protein; and diagnosing a Neisserial infection. NspA has
characteristics which indicate that it is a potential vaccine candidate
for the development of subunit vaccines for the treatment of infections
caused by Neisseria meningitidis (meningococcus), which causes invasive
caused by Neisseria meningitidis (meningococcus), which causes invasive
caused by Neisseria meningitidis (meningococcus), which causes invasive
caused by Neisseria be used to produce vaccine compositions and it could
space the development of produce vaccine compositions and it could
also be used in the development of new antimicrobial agents, diagnostic
tests and in drug screening. However, recombinantly produced proteins are
frequently unable to adopt their biologically active conformations, and
yields may be very low due to mis-folding and aggregation of the protein.
The method of the invantion provides an improved method for refolding the
conformation and it is possible to increase the recovery of active protein form partly purified inclusion bodies in amounts up to 100% without the need for further purification. The refolded NspA protein is useful for preparing a composition for diagnosing, treating or preventing infection caused by Neisseria meningitidis or Neisseria gonorrhoeae. The 480 GTCGATTTTGGATGCCGGCTACGCTACATCGGCAAAGTCAAAGACCAAAAAC present sequence represents the NspA gene from Neisseria meningitidis New refolded NspA protein, useful for preparing a composition for diagnosing, treating or preventing infection caused by Neisseria meningitidis or Neisseria gonorrheae.

481 GTCCGTTCCGGCGAACTGTCCGTCGGCGTGCAAATTCTGA 481 GTCCGTTCCGGCGAACTGTCCGTCGGCGTGCGCGTCAAATTCTGA

Composition comprising liposome associated with isolated polypeptide or polynucleotide derived from Neisseria meningitidis strain 608B, or its fragment or analog, useful for inducing an immune response against N.

The present invention relates to a pharmaceutical composition comprising a liposome associated with an isolated polypeptide derived from Neisseria meningitidis strain 608B, where the polypeptide is the Neph protein. The composition is useful for inducing an immune response against N meningitidis, for preventing and/or treating N. meningitidis infection and for treating and/or preventing neisserial infection chosen from N. meningitidis, N. gnorrhoaea, N. lactamica and N. polysacocharea. It is useful for treatment or prophylaxis of meningities and meningoccaemia, in a host. The host is a mammal, preferably a human and more preferably an adult human. The present sequence is the Neisseria meningitidis strain

Sequence 525 BP; 117 A; 186 C; 119 G; 103 T; 0 U; 0 Other;

0; Gaps Length 525; 0; Indels

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9 1 ATGAAAAAAGCACTTGCCACAGATTGCCCTCGCTCTCCCGGCCGCCGCACTGGCGGAA **ATGAAAAAAGCACTTGCCACACTGATTGCCCTCGCTCTCCCGGCCGCCGCACTGGCGGAA**

120 GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTTTTA 120 GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA

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120 262 180 322 240 382 300 442 360

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420 562 480 622

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A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen, antigenic fragments of antibodies can be used in a vaccine for the prevention of infection by N. meningitidis or by N. gonorrhoeae in humans. The antibodies may also be used diagnostically to detect N. meningitidis infection. The antigen may also be used to detect N. meningitidis antigen. DNA sequences encoding the antigen, or their fragments, can be used as probes for the detection of pathogenic Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
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Neisseria meningitidis antigen, highly conserved between different
strains - useful for prodn. of antibodies for immunisation against,
diagnosis of, N. meningitidis infection.
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                                                                                                                                                                                                                                           Length 830;
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100.0%; Pred. No. 5.3e-125;
iive 0; Mismatches 0;
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                                                      Claim 12; Fig 1; 117pp; English
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P-PSDB; AAW04891.
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Sequence 830 BP; 210 A; 261 C; 175 G; 184 T; 0 U; 0 Other;

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Neiserria meningitidis.
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US2002177551-A1.

28-NOV-2002.

30-MAY-2001; 2001US-00870759.

31-MAY-2000; 2000US-0208128P

(TERM/) TERMAN D S.

Terman DS;

WPI; 2003-361759/34. P-PSDB; ABU79079. A mammalian cell receptor, useful in the treatment of cancer by binding to tumor associated lipids where the binding induces anergy or apoptosis in T cells and antigen presenting cells.

Disclosure, Page, 167pp, English.

tree invention relates to a mammalian cell receptor, useful in the treatment of cancer, which binds to tumour associated lipids and induces anergy or apoptosis in the T cells and antigen presenting cells (APCs).

Also included are a mammalian cell useful in the treatment of cancer where the receptors which binds tumour associated lipids and induces cellular inactivation or death is debleted or functionally deactivated, producing (MI) a tumourcidal immunocyce population in vivo in a mammal producing (MI) a tumourcidal immunocyce population in vivo in a mammal (by allowing tumour associated lipids to context immunocyces in which creeptors for immunocyce and protecolycolipids, spuglosphingolipids, phosphosphingolipids, and and an animalian T cell settlement of cancer teratment of cancer comprising a superantisen (SAg) uncledied and inserted into a virus, a mammalian T cell settlement of cancer (where an adaptor protein which consistent in the treatment of cancer (where an adaptor protein which consistent in the treatment of cancer (comprising a lipid and composition useful in the treatment of cancer (comprising a lipid and composition and administering the tumouricidal limunocyce population are vivo in a mammal (by allowing tumour associated in immunocyce population and administering himmunocyce to produce a tumouricidal sumunocyce to produce a tumouricidal sumunocyce to produce a tumouricidal sumunocyce to the host, producing (WI) a tumour associated initiate and administering het unmouricidal summanal (by allowing a tumour associated lipids context cells, in which receptors for the tumour associated lipids to context T cells, and administering het unmouricidal population of a tumouricidal and an and and an and an antitumour associated antigens to context T cells of a tumouricidal T cell oppulation in vivo in a mammal (by allowing a tumouricidal T cell oppulation are uncontext in the present of administering and compositions are unequence and compositions are unequenced and compositions are unequenced and composi

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O III S	Query Match 100.0%; Score 525; DB 8; Length 830; Best Local Similarity 100.0%; Pred. No. 5.3e-125; Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ò	1 ATGAAAAAAGGGCTTGCCACACTGATTGCCCTCGCTCTCCGGGGCGGCGCACTGGCGGAA 60
셤	143 ATGAAAAAAGGACTTGCCACACTGATTGCCCTCGCTCTCCCGGCCGCCGCCGCACTGGCGGAA 202
ò	61 GGGGCATCCGGCTTTTACGTCCAAGCCGAAAAGCCTCAAGCTCTTTA 120
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\$ 6	121 GGTTCTGCCAAAGGCTTCAGCCGGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC 180 263 GGTTCTGCCAAAAGGCTTCAGCCATCTCCGCAAGACTCAACAACAACAACAACAACAACAAACA
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음 전	1110cCcfrcfrtfacacccccrtacaaactriacaaccccrtccacccarticaactriacaaccaaccaaccaaccaaccaaccaaccaaccaacc
ò	241 TACAGCATCGGCGCGTCCGCCATTTACGACTTCGACACCCCATCGCCCGTCAAACCGTAT 300
q	383 TACAGCATCGGCGATTTACGACTTCGACACTCGACCCGATCGCCCGTCAAACCGTAT 442
ò	301 CTCGCGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACTTGGGCGGCAGCGACGACGTC 360
qu	443 CTCGGCGCGCGCTTGAGCCTCCGCGCCTCCGTCGACTTGGCGCGCGAGCGA
ò	361 AGCCAAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAAGCCGTTACCCCGAAT 420
අධ	503 AGCCAAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAAGCTATGCCGTTACCCCGAAT 562
λŏ	421 GTCGATTTGGATGCCGGCTACCGCTACACTACGGCAAAGTCAACACTGTCAAAAC 480
qu	563 GICGALTIGGAIGCCGGCTACCGCTACATCGGCAAAGTCAACACTGTAAAAC 622
λŏ	481 GTCCGTTCCGGCGAACTGTCCGTCGGCGTCAAATTCTGA 525
ପ୍ର	623 GTCCGTTCCGGCGAACTGTCCGTCGGCGTCACATTCTGA 667
RES ADF ID	RESULT 5 ADF43315 ID ADF43315 standard: DNA: 830 BP.
A XX	315;
XE:	12-FEB-2004 (first entry)
等品	N. meningitidis lipopolysaccharide DNA seq id 35.
{	receptor; lipid-based tumour associated antigen; cytostatic; antimicrobial; gene therapy; neoplastic disease; tumour; cancer; infectious disease; lipopolysaccharide; LPS; ds.
\$8 \$	Neisseria meningitidis.
{ Z }	US2003157113-A1.
₹ B \$	21-AUG-2003.
PF	28-DEC-2000; 2000US-00751708.
PR	28-DEC-1999; 99US-0173371P.
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                                                                                                          The invention describes a receptor in a mammalian cell that inhibits regular activation by receptors specific for lipid-based tumour associated antigen. The receptor has cytostatic and antimicrobial properties and is suitable for use in gene therapy. The receptors, methods and compositions are useful for treating a neoplastic disease or tumour (cancer), and infectious diseases. This sequence encodes Neisseria meningitidis lipopolysaccharide (LPS) to which tumour cells develop
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                                                                                                                             Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine;
diagnosis; antigen; detection; infection; gene therapy; antibacterial;
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Scarselli M,
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ti C, Mora M, Ratti G,
CM, Grandi G;
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28-FEB-2000; 2000GB-00004695.
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Masignani V, Galeotti C
Rappuoli R, Frazer CM,
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The present invention describes the full length genome of Neisseria
meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
CC represent fragments of the NMB genomic sequence, as the sequence was too
long to go in a record on its own it was split into 8 sequences which
co verlap each other at the beginning and end of each sequence by 49980 bp
(i.e. the last 49980 bp of AAF21541 is repeated at the beginning of
AAF21607, the last 49980 bp of AAF21507 are repeated at the beginning of
AAF21608, and so on). AAF21545 to AAF21589 encode the Neisseria proteins
CC AAF21608, and so on). AAF21545 and AAF21580 encode the Neisseria proteins
CC AAF21609, and so on). AAF21545 to AAF21580 encode the Neisseria proteins
CC AAF21609, and so on). AAF2164 is respeated at the beginning of
AAF21609, and so on). AAF2164 is respeated at the beginning of
CC AAF21609, and so on). AAF2164 is complification of the present invention.
CC AAF21609, and so on). AAF2164 is completed a city of the proteins and can
CC The NMB genome and fragments from it have antibacterial activity, and can
CC The NMB genome and gene therapy. Neisserial bacteria or as a
diagnostic reagent for detecting the presence of Neisserial bacteria or
CC antibodies raised to Neisserial bacteria.
CC antibodies raised to Neisserial bacteria or sed
CC dentify open reading frames (ORFS) or coding sequences within the NMB
CC dentify open reading frames (ORFS) or coding sequences within the NMB
CC outer membrane proteins which are more effective in vaccines than the
CC outer membrane proteins which are more effective in vaccines than the
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Neisseria meningitidis B full length genome sequence and open reading frames are used to detect, treat and prevent Neisserial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90726 GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 349980 BP; 82523 A; 82940 C; 96712 G; 87805 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGAAAAAGCACTTGCCACACTGATTGCCCTCGCTCTCCCGGCCGCCGCACTGGCGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 99.4%; Score 521.8; DB 3; Length 349980; Best Local Similarity 99.6%; Pred. No. 1.4e-123; Matches 523; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCCGTTCCGGCGAACTGTCCGTCGGCGTGCGCGTCAAATTCTGA 525
                                                                                                                        Claim 7; Appendix A; 692pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301
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AAT39041 standard; DNA; 850

360 567 420 627 480 687

507

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The present invention relates to a new gram-negative bacterial bleb presenting on its surface the PorB outer membrane protein from Chlamydia trachomatis, or a protective antigen from C. pneumoniae. The invention is useful for preventing C. trachomatis or C. pneumoniae infection in a host. The present nucleic acid sequence represents a Neisseria gonorrhoeae gene as described in the invention
388 TTCGCCGTCGATTACACGCGCTACAAAACTATAAAGCCCCATCCACCGATTTCAAACTT 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel gram-negative bacterial bleb presenting on its surface PorB outen membrane protein from Chlamydia trachomatis or protective antigen from Chlamydia pneumoniae, useful for preventing Chlamydia infection.
                                                           TACAGCATCGGCGTCCGCCATTTACGACTTCGACACCCCAATCGCCCGTCAAACCGTAT
                                                                                                                       CTCGGCGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACTTGGGCGGCAGCGACAGCTTC
                                                                                                                                            CTCGGCGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACTTGGGCGCACAGCAACCAGCTTC
                                                                                                                                                                                                    361 AGCCAAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAAGCTATGCCGGTTACCCCGGAT
                                                                                                                                                                                                                                    AGCCAAACTCCACCGGCCTCGGCGTATTGGCGGGCGTAAGCTATGCCCGTTACCCCGAAT
                                                                                                                                                                                                                                                                                     GTCGATTTGGATGCCGGCTACCGCTACAACTACATCGGCAAAGTCAACACTGTCAAAAAC
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Chlamydia trachomatis infection; Chlamydia pneumoniae infection;
protective antigen; antibacterial; vaccine; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                         0 Other;
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                                                                                                                                                                                                                                                                                                                                                                    GTCCGTTCCGGCGACTGTCCGTCGCGTGCGCGTCAAATTCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 95.7%; Score 502.6; DB 6; Best Local Similarity 97.3%; Pred. No. 2.9e-119; Matches 511; Conservative 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3erthet FJ, Lobet Y, Poolman J, Verlant VGCL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria gonorrhoeae outer membrane gene #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 54; 75pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen, antigent fragments of antibodies can be used in a vaccine for the prevention of infection by N. meningitidis or by N. gonorrhoeae in humans. The antibodies may also be used diagnostically to detect N. meningitidis infection. The antigen may also be used to detect antibodies specific to N. meningitidis antigen. DNA sequences encoding the antigen, or their fragments, can be used as probes for the detection of pathogenic Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
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                                                                                                                                                         reistant; Neisseria meningitidis; Neisseria gonorrhoeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis antigen, highly conserved between different
strains - useful for prodn. of antibodies for immunisation against,
diagnosis of, N. meningitidis infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.8%; Score 518.6; DB 2; Length 850; 99.2%; Pred. No. 2.3e-123; Pred. 0; Mismatches 4; Indels 0;
                                                                                                                   Proteinase K resistant N. meningitidis 22 kD surface protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 850 BP; 208 A; 273 C; 185 G; 184 T; 0 U; 0 Other;
                                                                                                                                                                                 antibody; detection; probe; surface protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rioux C;
                                                                                                                                                                                                                   Neisseria meningitidis; strain 24063
                                                                                                                                                                                                                                                               Location/Qualifiers
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95US-0001983P,
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                                                                            (first entry)
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265. .729
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Matches 521; Conservative
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                                                           (revised)
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P-PSDB; AAW04893.
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                                                       16-OCT-2003
22-DEC-1996
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Neisseria meningitidis antigen, highly conserved between different strains - useful for prodn. of antibodies for immunisation against, diagnosis of, N. meningitidis infection.
                                                                    Claim 12; Fig 10; 117pp; English.
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(first entry)
       WPI; 1996-443187/44.
P-PSDB; AAW04894.
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22-DEC-1996
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                                           TTCGCCGTCGATTACACGCGCTACAAAACTATAAAGCCCCATCCACCGATTTCAAACTT
                                                                                                                 TTCGCCGTCGATTACACGCGCTACAAAAACTATAAAGCCCCATCCACCGATTTCAAACTT
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                                   GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA
                                                                    GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC
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antibody; detection; probe; surface protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                           Proteinase K resistant N. meningitidis 22 kD surface protein
                                                                                                                                                                                                                                                                                   GTCCGTTCCGGCGAACTGTCCGTCGGCGTGCGCGTCAAATTCTGA 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rioux C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis; strain b2.
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95US-0001983P.
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241. .297
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298. .762
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04-AUG-1995;
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22-DEC-1996
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A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen, antigenic fragments of antibodies can be used in a vaccine for the prevention of infection by N. meningitidis or by N. gonorrhoeae in humans. The antibodies may also be used diagnostically to detect N. meningitidis infection. The antigen may also be used to detect antibodies specific to N. meningitidis antigen. DNA sequences encoding the antigen or thair fragments, can be used as probes for the detection of pathogenic Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                   Score 502.6; DB 2; Length 810;
Pred. No. 3e-119;
0; Mismatches 14; Indels 0;
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                                                                                                                                                                                                                                                                       Sequence 810 BP; 186 A; 260 C; 186 G; 178 T; 0 U; 0 Other;
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Best Local Similarity 97.3%;
Matches 511; Conservative
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The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae linfection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABZ37706-ABZ42016 represent nucleic acid molecules of the invention
                                                                                      AATGTCGATTTGGATGCCGGCTACCGCTACAACTACATCGGCAAAGTCAACACTGTCAAA
                                                                                                                                                                536 AATGTCGATTTGGATGCCGGCTACCCTACAACTACATCGGCAAAGTCAACACTGTCAAA
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                                                         TTCAGCCAAACCTCCATCGGCCTCCGCCTATTGACGGCGTAAGCTATGCCCCC
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                                                                                                                                                                                                          AACGTCCGTTCCGGCGAACTGTCCGTCGGCGTGCGCGTCAAATTCTGA
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Pred. No. 1.5e-113;
0; Mismatches 18; Indels
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Best Local Similarity 96.0%;
Matches 504; Conservative
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                       e K reistant; Neisseria meningitidis; Neisseria gonorrhoeae; detection; probe; surface protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis antigen, highly conserved between different
strains - useful for prodn. of antibodies for immunisation against,
diagnosis of, N. meningitidis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 710 BP; 174 A; 232 C; 148 G; 156 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 491.2; DB 2
Pred. No. 2.5e-116
0; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rioux
                                                                             Neisseria meningitidis; strain MCH88.
                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Fig 8; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Martin D, Hamel
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95US-0001983P
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                                                                                                                                   116. .643
/*tag= a
116. .172
/*tag= b
173. .640
/*tag= c
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Matches 512; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     (IAFB-) IAF BIO VAC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-443187/44.
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04-AUG-1995;
                                                                                                                                                                                                                                                                                                                                          15-MAR-1996;
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                         Proteinase
                                        antibody;
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                                                                                                                                                                       301 TATTTCGGCGCGCGCTTGAGCCTCAACCGCGCTTCCGCCCACTTGGGCGGCGCAGCGACAGC 360
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                                                                                                                                                                                                                                                                        421 AATGTCGATCTGGATGCCGGCTACCGCTACAACTACGTCGGCAAAGTCAACAATGTCAAA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisserial surface protein A; NspA; refolding; recombinant production;
               GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC
                                                                TTGGCCGTCGATTACACGCGCTACAAAACTATAAACAAGCCCCATCCACCGATTTCAAA
                                                                                                                                                TATCTCGGCGCGCGCTTGAGCCTCAACCGCGCTCCGTCGACTTGGGCGGCGGCGACAGC
                                                                                                                                                                                                 TTCAGCCAAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAAGCTATGCCGTTACCCCG
                                                 TTCGCCGTCGATTACACGCGCTACAAAACTATA----AAGCCCCATCCACCGATTTCAAA
                                                                                                CTTTACAGCATCGGCGTCCGCCATTTACGACTTCGACACCCAATCGCCCGTCAAACCG
                                                                                                                         CTTTACAGCATCGGCGCGTCCGTCATTTACGACTTCGACACCCAATCGCCCGTCAAACCG
                                                                                                                                                                                                                                                 AATGTCGATTTGGATGCCGGCTACCGCTACAACTACATCGGCAAAGTCAACACTGTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine; subunit vaccine; prevention; diagnosis; meningococcus; invasive bacterial disease; bacteraemia; meningitis; Neisseria gonorrhoea; gonorrhoea; antibacterial; gene therapy; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Poolman J;
                                                                                                                                                                                                                                                                                                 AACGTCCGTTCCGGCGAACTGTCCGTCGGCGTGCGCGTCAAATTC 522
                                                                                                                                                                                                                                                                                                               AACGTCCGTTCCGGCGAACTGTCCGCCGCGCGTCGAATTC 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis H44/76 mature NspA-encoding DNA
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/product= "Mature NspA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feron C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/product= "Mature NspA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis; H44/76.
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                                                                                                                                                                                                                                                                                                                                                                                      ADL13425 standard; DNA; 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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P-PSDB; ADL13426.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUN-2004
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The invention relates to an insolated related with selection to the invention relates to the method of refolding an NspA protein; an invention also relates to the method of refolding an NspA protein; and invention also relates to the method of refolding an NspA protein; and dimethyldodecylammoniopropanegulphonate) for refolding an NspA protein, a dimethyldodecylammoniopropanegulphonate) for refolding an NspA protein, a carrier and optionally one or more other Neisserial antigens; a method of preventing or treating a Neisserial infection. NspA has contracteristics which indicate that it is a potential vaccine candidate for the development of subunit vaccines for the treatment of infections caused by Neisseria meningitidis (meningococcus), which causes invasive consed by Neisseria meningitidis (meningococcus), which causes invasive consed by Neisseria meningitidis (meningococcus), which causes invasive conservable development of genorathoea. Recombinantly produced conformations and it could also be used in the development of new antimicrobial agents, diagnostic tests and in drug screening. However, recombinantly produced proteins are frequently unable to adopt their blologically active conformations, and yields may be very low due to mis-folding and aggregation of the protein. The method of the invention provides an improved method for refolding the NSPA protein, and it is possible to increase the recovery of active protein form partly purified inclusion bodies in amounts up to 100% without the need for further purification. The refolded NsPA protein is useful for preparing a composition for diagnosing, treating or preventing cuseful for preparing a composition for diagnosing, treating or preventing infection caused by Neisseria meningitidis or Neisseria generation expense. The
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                                                                                                                                                          invention relates to an isolated refolded Neisserial surface protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present sequence represents DNA encoding the mature NspA protein from Neisseria meningitidis H44/76 which was amplified and cloned in an example of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CGCTTCGCCGTCGATTACACGCGCTACAAAACTATAAAGCCCCATCCACCGATTTCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                     New refolded NspA protein, useful for preparing a composition foi
diagnosing, treating or preventing infection caused by Neisseria
meningitidis or Neisseria gonorrheae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 468 BP; 105 A; 164 C; 106 G; 93 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 464.8; DB 12
Pred. No. 1.4e-109;
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                                                                                                             Example 1; Fig 2; 62pp; English
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AACGICCGITCCGGCGAACTGICCGCCGGTGTGCGCGTCAAATTCTGA

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New protein from Neisseria gonorrheae, useful for the manufacture of a medicament for treating or preventing N. gonorrheae infection.
                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 486 BP; 101 A; 107 C; 168 G; 110 T; 0 U; 0 Other;
                                                                                Antibacterial; infection; vaccine; gene therapy; gene; ds.
                                                               N. gonorrhoeae nucleotide sequence SEQ ID 2509.
                                                                                                                                                                                                                   Monaci E;
                                                                                                                                                                                                                                                                                            Disclosure; Page 371; 815pp; English
                                                                                                                                                                                                                  Masignani V,
       ABZ38960 standard; DNA; 486 BP
                                                                                                                                                          12-FEB-2002; 2002WO-IB002069.
                                                                                                                                                                             12-FEB-2001; 2001GB-00003424.
                                                                                                                                                                                                                 Fontana MR, Pizza M,
                                                                                                    Neisseria gonorrhoeae
                                                                                                                                                                                                                                    WPI; 2003-058415/05.
P-PSDB; ABP77990.
                                                                                                                                                                                                (CHIR-) CHIRON SPA
                                                                                                                      WO200279243-A2
                                            07-MAR-2003
                                                                                                                                        10-OCT-2002
                         ABZ38960;
ABZ38960/c
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180 AATGTCGATTTGGATGCCGGCTACCGCTACAACTACATCGGCAAAGTCAACACTGTCAAA 477 427 237 426 TTCGCCGTCGATTACACGCGCTACAAAAACTATAAACAAGCCCCATCCACCCGATTTCAAA 367 CTTTACAGCATCGGCGTCCGTCATTTACGACTTCGACACCCAATCGCCCGTCAAACCG 307 TATCTCGGCGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACTTGGGCGGCAGCGACAGC 357 247 TTCAGCCAAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAAGCTATGCCGTTACCCCG 417 CITTACAGCATCGGCGCTCCGCCATTTACGACTTCGACACCCAATCGCCCGTCAAACCG 297 The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABZ37706-ABZ42016 represent nucleic acid molecules of the invention TATTTCGGCGCGCGCTTGAGCCTCAACCGCGCTTCCGCCCACTTGGGCGGCAGCGACAGC GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC 486 GGTTCTGCCAAAGGCTTCAGCCCGCGTTCTCCGCAGGCTACCGCATCAACGACCTCCGC TTCGCCGTCGATTACACGCGCTACAAAACTATA---AAGCCCCATCCACCGATTTCAAA 3; Gaps Score 368; DB 10; Length 486; Pred. No. 1e-84; 0; Mismatches 15; Indels Query Match 70.1%; Best Local Similarity 95.6%; Matches 390; Conservative C 306 181 238 366 298 358 418 g g a g g ઠે 8 8 à ò

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186 AATGTCGATCTGGATGCCGGCTACCGCTACAACTACGTCGGCAAAGTCAACAATGTCAAA 12	478 AACGICCGTICCGGCGAACTGTCCGCCGTGCGCGTCCAAATTCTGA 525	126 AACGICCGTICCGGCGAACIGICCGCCGGCGGGCGGCGTCAAATICTGA 79	
186	478	126	
QΩ	δ	д	

Search completed: May 19, 2005, 15:25:55 Job time : 1070 secs

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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
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TELEX: 90416
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 830 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
Sequence 1, Appli
Sequence 5, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 175, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 363, Appli
Sequence 71, Appli
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Sequence 374, App
Sequence 15, Appl
Sequence 2, Appli
Sequence 6, Appli
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Sequence 11, Appl
Sequence 340, App
                                                                                                                                                                       May 19, 2005, 15:26:04 ; Search time 540 Seconds (without alignments) 1590.825 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*
(cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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(cgn2_6/ptodata/1/ina/6B_COMB.seq:*
(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-913-362-5

US-08-913-362-29

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US-08-913-362-29

US-08-913-362-3

US-09-103-840A-2

3 US-09-103-840A-1

3 US-09-103-840A-1

3 US-09-103-840A-1

US-09-103-840A-1

US-09-107-649-7

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US-09-902-540-1169

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Maximum Match 100%
Listing first 45 summaries
                                                                                                                         - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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525
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Match Length
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                    Sequence:
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29 41.6 7.9 1877 08.0-21.2-33B-342 Sequence 343. App 10.0-21.2-33B-345 Sequence 343. App 10.0-21.2-33B-345 Sequence 345. App 10.0-21.2-33B-345 Sequence 346. App 10.0-21.2-32B-365 Sequence 346. App 10.0-21.2-32B-365 Sequence 346. App 10.0-21.2-32B-365 Sequence 346. App 10.0-21.2-32B-365 Sequence 34. App 10.0-224 4 US-0-2-26-123 Sequence 123. App 10.0-224 4 US-0-2-26-123 Sequence 123. App 10.0-224 4 US-0-2-26-126 Sequence 17. App
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GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 TACAGCATCGGCGGTCCGCCATTTACGACTTCGACACCCAATCGCCCGTCAAACCGTAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 CTCGGCGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACTTGGGCGGCAGCGGACAGCTTC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCGGCGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACTTGGGCCGCGCGGCAGCAACCTTC 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 ATGAAAAAGCACTTGCCACACTGATTGCCCTCGCTCTCCCGGCCGCCGCACTGGCGGAA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 TTCGCCGTCGATTACACGCGCTACAAAAACTATAAAGCCCCCATCCACCGATTTCAAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               448 TACAGCATCGGCGGTCCGCCATTTACGACTTCGACACCCAATCGCCCGTCAAACCGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGAAAAAAGCACTTGCCACACTGATTGCCCTCGCTCTCCCGGCCGCCGCACTGGCGGAA
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Pred. No. 3e-136;
0; Mismatches 4; Indels 0
                                                   MEDIUM TYPE: Riopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
PILING DATE: 13-NOV-1997
PRIOR APPLICATION NUMBER: US 08/406,362
PILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: US 08/406,362
PILING DATE: 04-AUG-1995
ATPONEY/AGENT INPORMATION:
APPLICATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REBERENCE/DOCKET NUMBER: 047998/0128
TELEPPAK: (202)672-5309
THELEPPAK: (202)672-5309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Neisseria meningitidis STRAIN: Z4063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.2%;
Matches 521; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 904136
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 850 base pairs
TYPE: mucleic acid
STRANDEDNESS: double
                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sig_peptide
208..264
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCCAAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAAGCTATGCCGTTACCCCCGAAT 420
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| Patent No. 6287574
| GENERAL INFORMATION:
| APPLICANT: Brodeur, Bernard R
| APPLICANT: Martin, Denis
| APPLICANT: Hamel, Josee
| APPLICANT: Hamel, Josee
| APPLICANT: Rioux, Clement
| TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
| NUMBER OF SEQUENCES: 30
| CORRESPONDENCE ADDRESS:
| ADDRESSE: Poley & Lardner
| STREET: 3000 K Street, N.W., Suite 500
| CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 4.8e-138;
Matches 525; Conservative 0; Mismatches 0; Indels
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ORIGINAL SOURCE:
ORGANISM: Neisseria meningitidis
STRAIN: 608B
                                                                                                                                                           sig_peptide
143..199
                                                                                                                                                                                                                             mat_peptide 200..667
                                                                                           CDS
143..667
                                                             FEATURE:
NAME/KEY:
LOCATION:
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LOCATION:
FEATURE:
                                                                                                                                                                                                                          ; NAME/KEY:
; LOCATION:
US-08-913-362-1
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US-08-913-362-5
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                                                                                                                                                                 1 ATGAAAAAAGCACTTGCCAÇACTGATTGCCCTCGCTCTCCCGGCCGCCGCACTGGCGGAA
                                                                                                                            Gaps
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US-08-913-362-29

US-08-913-362-29

Sequence 29, Application US/08913362

Sequence 29, Application US/08913362

Sequence 29, Application US/08913362

Sequence 20, Application US/08913362

Sequence 20, Application US/08913362

APPLICANT: Brodent, Bernard R

APPLICANT: Hamel, Josee

APPLICANT: Hamel, Josee

APPLICANT: Rioux, Clement

TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN

TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & Lardner

STREET: 3000 K ****

CITV.
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                                                                                   Length 810;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
                                                                                Score 502.6; DB 3;
Pred. No. 9.5e-132;
0; Mismatches 14;
                                                                                95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                      Best Local Similarity 97.3
Matches 511; Conservative
mat_peptide
298..765
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STATE: D.C.
COUNTRY: US
; NAME/KEY:
; LOCATION:
US-08-913-362-7
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                                           568 AGCCAAACCTCCACCGGCCTCGGCGTATTGGCGGGCGTAAGCTATGCCGTTACCCCGAAT 627
                                                                                     GTCGATTTGGATGCCGGCTACCGCTACAACTACATCGGCAAAGTCAACACTGTCAAAAAC 480
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
                                                                                                                                                                                              GTCCGTTCCGGCGAACTGTCGCCGGTGTGCGCGTCAATTCTGA 732
                                                                                                                                                                        GTCCGTTCCGGCGAACTGTCCGTCGGCGTGCGCGTCAAATTCTGA 525
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ZIP: 20007-5109

COMPUTER READBABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN DATA:

APPLICATION NUMBER: US/08/913,362

FILING DATE: 13-NOV-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/406,362

FILING DATE: 17-NAR-1995

FILING DATE: 17-NAR-1995

FILING DATE: 17-NAR-1995

FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REGISTRATION NUMBER: 29,768

TELERHONE: (202)672-500

TELERHONE: (202)672-500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3000 K Street, N.W., Suite 500 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Neisseria gonorrhoeae
STRAIN: b2
                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08913362
Patent No. 6287574
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 810 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sig_peptide 241..297
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ADDRESSEE: Foley & L
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LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
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                   TITLE OF INVENTION: DEPOTEINAGE K RESISTANT SURFACE PROTEIN TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS NUMBER OF SEQUENCES: 30 CORRESPONDENCE ADDRESS: ADDRESSE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C. COUNTRY: USA CONTRY: USA ZIP: 20007-5109 COMPUTER READABLE FORM: MEDING TYPE: Floppy disk.
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                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
ATTORNEY/AGENT INFORMATION:
NAME: Bent. Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (202)672-5309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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TELEFAX: (202,
TELEX: 904136
; INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 710 base pairs
""PE: mucleic acid
""PE: mucleic acid
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ORIGINAL SOURCE:
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LOCATION:
FEATURE:
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FEATURE:
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95.5%; Score 501.2; DB 3; Length
Best Local Similarity 95.1%; Pred. No. 2e-131;
Matches 502; Conservative 22; Mismatches 1; Indels
                   APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
RICH APPLICATION DATA: 3 TO A PRICATION DATA: 3 TO A PRICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY, FAGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEFRAX: (202)672-5300
TELEFAX: (202)672-5399
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US-08-913-362-3
US-08-913-362-3
; Sequence 3, Application US/08913362.
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other nucleic acid /desc = "consensus"
                                                                                                                                                                                                                                                                                                                                      TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 528 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
PRIOR APPLICATION DATA:
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456 CCGTCGACCTCCAGTCCCTCTGCTTCTACTCCGCGCCCAAGACCAAGCCCAAGCTCAACA 515
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LENGTH: 4403765
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                                                                                               CTTTACAGCATCGGCGCTCCGCCATTTACGACTTCGACACCCCAATCGCCCGTCAAACCG
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49.8%; Pred. No. 0.00035;
iive 0; Mismatches 127; Indels 0
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TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB1378 US NA
CURRENT APPLICATION NUMBER: US/09/614,912
CURRENT FILING DATE: 2000-07-12
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PRIOR FILING DATE: 1999-07-12
PRIOR PELING DATE: 1999-07-12
PRIOR PELING DATE: 1999-07-30
PRIOR PILING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR PILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/172,946
PRIOR PILING DATE: 1999-12-21
NUMBER PILING DATE: 1999-12-21
SOFTWARE: MISCOSOFT OF 12-21
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Lee, Jian Ming
Sakai, Hajime
Weng, Zude
Caimi, Perry G
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PRIOR FILING DATE: 1999-07-12
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Rafalski, Antoni
Orozco, Buddy
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ORGANISM: Triticum aestivum
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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Facent No. 6294328

GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: PRASER, Claire M.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1 GCATCGGCGCGTCCGCCATTTACGACTTCGACACCCCAATCGCCCGTCAAACCGTATCTCG 304 FEATURE:

OTHER INFORMATION: CDC 1551

OTHER INFORMATION: "n" bases at various positions throughout the sequence
COTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2 70 GGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTAGGTTCTGCC 190 GATTACACGCGCTACAAAACTATAAAGCCCCATCCACCGATTTCAAACTTTACAGCATC 10 GCACTTGCCACACTGATTGCCCTCGCTCTCCCGGCCGCCACTGGCGGAAGGCGCATCC 3731518 GCGGCCGGCGCCGTTGCCGCCGAAGGCCGCCATTGCCTTCGGGGCCTCCCGGACCGCC 130 AAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGCTTCGCCGTC 8.7%; Score 45.6; DB 3; Length 4403765; 44.6%; Pred. No. 0.094; tive 0; Mismatches 224; Indels 0;

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426711 AÁCTACAACACCGGCTTGCTC 426691
                    LENGTH: 4403765
TYPE: DNA
OKGANISM: Mycobacterium tuberculosis
PEATURE:
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APPLICANT: FLEISCHMAN, ROBERT D. APPLICANT: WHITE, Owen R.
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Best Local Similarity 44.9%;
Matches 171; Conservative
                                                                                                                                                                                                                                                                         Best Local Similarity 44.9
Matches 171; Conservative
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SEQ ID NO 2
                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 GCACTIGCCACACTGAITGCCCTCGCTCTCCCGGCCGCCGCACTGGCGGAAGGCGCATCC 69
                                                                                                                                                                                         APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Patent No. 6294328

RAGENEAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WINTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION WUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45.6; DB 3; Length 4 Pred. No. 0.095; 0; Mismatches 224; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
                                                                        Application US/09103840A
                                                                     Sequence 1, Application US/091038
Patent No. 629431038
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 44.6%;
Matches 180; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1
LENGTH: 4411529
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US-09-103-840A-2/c
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                                           JS-09-103-840A-1
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                                                                                                                                                                                                                                                                                                                               133 GGCTTCAGCCCGCGCATCTCCCGCAGGCTACCGCATCAACGACCTCCGCTTCGCCGTCGAT 192
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 TACACGCGCTACAAAAACTATAAAGCCCCATCCACCGATTTCAAACTTTACAGCATCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313 TTGAGCCTCAACCGCGCCCTCCGTCGACTTGGGCGGCAGCGACACGTTCAGCCAAACCTCC
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APPLICANT: FRASER, Claire M.
APPLICANT: VERSER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REPERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                              Score 45; DB 3; Length 4403765;
Pred. No. 0.14;
0; Mismatches 210; Indels 0;
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Pred. No. 0.14;
0; Mismatches 210; Indels
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Sequence 363 Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
THE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2839 Aceaerecricescrichecarcaaceaerecercaecercaecaacacarcaecric 2898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --CGACTTCGACACCCAATCGCCCGTCAAACCGTATCTCG 304
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102 GCCTCGCCGCGCGCGCTACCTCGGCCTCGACACACATCCCGCACTCGGCCATCGGC 761
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                                                                                                                                                                  Score 44; DB 3; Length 448
Pred. No. 0.021;
0; Mismatches 185; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSEE: Human Genome Sciences, Inc. F: 9410 Key West Avenue Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY GABNT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCS/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  822 CTCCTCATCAAGGCCCTCATCGAC 845
                                                                                                                                                                                                                                                                                                                                                                                      331 TCCGTCGACTTGGGCGGCAGCGAC 354
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
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Best Local Similarity 47.3%;
Matches 174; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: 1
STATE:
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OTHER INFORMATION: Organophosphate Hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126733 GGCTTCGGCGTCGGCCTATCCGGCGACACCAGGTGGGCATCGGCGCACCCAACTCGGGC 426574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               426613 ACCGGCAACGTCGGCATCGGCAACACCCGGCAACACCCGGCATCGGAAAACAGCGGC 426554
                                                                                                                                                                        426853 AACACCGGTTTCTTCAACTCCGGCACCGCCAACACCGGCTTGTTCAACTCCGGCACGGC 426794
                                                                                                                                                                                                                                                                                                                                                                                426793 AACACCGGCTTGTTCAACTCGGGCACCGGCAACGTCGGCATCGGCAACATGGGCACCGGC 426734
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HOWARD, JOHN
APPLICANT: HOWARD, JOHN
APPLICANT: GASTEL, FRANS VAN
APPLICANT: WANG, HUAMING
APPLICANT: WAND, MICHAEL
APPLICANT: WOODARD, SUGAN
ITILE OF INVENTION: METHOD OF INCREASING RECOVERY OF HETEROLOGOUS ACTIVE
ITILE OF INVENTION: METHOD OF INCREASING RECOVERY
ITILE OF INVENTION: METHOD OF INCREASING RECOVERY
CURRENT APPLICATION NUMBER: US/09/881,165
CURRENT FILING DATE: 2001-06-14
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 5
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                                                                                                                                                                                                                                                                               312
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                                                                                                                                                                                                                                                                               253 GCGTCCGCCATTTACGACTTCGACACCCAATCGCCCGTCAAACCGTATCTCGGCGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   433 GCCGGCTACCGCTACAACTACATCGGCAAAGTCAACACTGTCAAAAACGTCCGTTCCGGC
                                                                           TACACGCGCTACAAAACTATAAAGCCCCATCCACCGATTTCAAACTTTACAGCATCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 175; Indels
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Patent No. 6632930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similaricy
Matches 149; Conservative
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1682 GAATCTGCATCAACCAGTGCGTCCGCTTCAGCGTCAACCAGTGCGTCGGCTTCAGCGTCG 1741
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CURRENT APPLICATION NUMBER: 07/829,461
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: 07/739,055
EARLIER PILING DATE: 1991-08-01
EARLIER APPLICATION NUMBER: 07/561,968
EARLIER FILING DATE: 1990-08-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PARENTIN Ver: 2.0
SEQ ID NO 7
ELENGRIER 390
                                                                                                                                                               ATTTGGATGCCGGCTACCGCTACAACTACATCGGCAAAGTCAACACTGTCAAAAACGTCC 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43.6; DB 3; Length 390;
Pred. No. 0.011;
0; Mismatches 199; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/09197649 Patent No. 6194550
                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Patent No. 6194550
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry
; APPLICANT: Tuerk Craig
; APPLICANT: Pribnow, David
; APPLICANT: Smith, Jonathan D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 45.0%;
Matches 163; Conservative
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                                                                                                                                                                                                                                                                                                                                                          Sequence 71, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                 2899 GAATCIGCATCAACCAGTGCGICCGCTTCAGCGICCAACCAGTGCGTCGGCTTCAGCGICG 2958
                                                                                                                                                            2959 ACAAGTGCTTCGGCTTCAGCATCAACGAGTGCGTCGGCCTCAGCAAAGCGCAAGTACCTCA 3018
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                        365 AAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAAGCTATGCCGGTTACCCCGAATGTCG 424
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                                                                                                              425 ATTIGGAIGCCGCCTACCACTACAACTACAACGTCAACACTGTCAAAAACGICC
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ilarity 47.3%; Pred. No. 0.043;
Conservative 0; Mismatches 185; Indels
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
CORRATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFRENCE/DOCKET NUMBER: PB34
TELEPHONE: (301) 309-8514
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 33768 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                     3019 GCGTCAGC 3026
                                                                                                                                                                                                          485 GTTCCGGC 492
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Best Local Similarity
Matches 174; Conserva
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Search completed: May 19, 2005, 20:34:02 Job time : 565 secs
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APPLICANT: Stassi, Diane L.
APPLICANT: Summers Jr., Richard G.
APPLICANT: Ruan, Xiaoan
APPLICANT: Pereda-Lopez, Ana
APPLICANT: Kakavas, Stephan J.
TITLE OF INVENTION: NOVEL POLYKETIDE DERIVATIVES
NUMBER OF SEQUENCES: 34
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8.2%; Score 43; DB 3; Length 925;
Best Local Similarity 44.3%; Pred. No. 0.022;
Matches 175; Conservative 0; Mismatches 220; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTE: 18064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,003
FILING DATE: 16-MAY-1979
CLASSIFFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Dianne Casuto
REGISTRATION NUMBER: P-40,943
REFERENCE/DOCKET NUMBER: 4952.US.P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847)-938-3137
TELEFAX: (847)-938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Abbott Laboratories
100 Abbott Park Rd.
                                                                                                                                                                        Sequence 1, Application US/08858003
Patent No. 6060234
GENERAL INFORMATION:
APPLICANT: Katz, Leonard
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SEQUENCE CHARACTERISTICS:
LENGTH: 925 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
JOPOLOGY: linear
US-08-858-003-1
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COUNTRY: USA
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                           GenCore version
Copyright (c) 1993 - 2005
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/clone lib="ADIO"
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/note="Organ: seedlings inoculated with Gluconacetobacter diazotroficans; Vector: pSportl, Site 1: Sall, Site 2:
Notl, An unidirectional cDNA library generated from lesedlings inoculated with Gluconacetobacter diazotroficans] cDNA was prepared from polyA+ mRNA using Supersoript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details
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SCAGAD1074C04.g AD1 Saccharum officinarum cDNA clone SCAGAD1074C04
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OSIFCC025
BJ748832
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WS1 9 E10
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AGENCOURT
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Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137

Fax: 55 19 3788 1089
Email: parrudaéunicamp.br
Email: parrudaéunicamp.br
Clone distribution: clone distribution information can be found thtp://www.bccenter.fcav.unesp.br
http://www.bccenter.fcav.unesp.br
Plate: 074 row: C column: 04
Seq primer: 17 Pronocter Primer.
Location/Qualifiers
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CB81064
CL978483
BJ748832
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CC57648
CX167632
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/organism="Saccharum officinarum"
/mol type="mRNA"
/db xref="taxon:4547"
/clone="SCAGAD1074C04"
/lab_host="DH10B"
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Vettore, A.L., da Silva, F.R., Kemper, E.L.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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Plate: 003 row: E column: 05
Seq primer: T7 Promoter Primer.
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of each source of RNA and library construction can b obtained at http://sucest.lad.ic.unicamp.br/public"
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Vettore, A.L., da Silva, F.R., Kemper, B.L. and Arruda, P. The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
                                                                                                                                              Length 622;
                                                                                                                                      Score 57.8; DB 6; Length.6 Pred. No. 4.3e-05; 0; Mismatches 192; Indels
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Caixa Postal 6010, 13083-970, Campinas SP,
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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Best Local Similarity 47.4%;
Matches 173; Conservative
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CA193415
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FEATURES

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/clone_lib="FL]"
//olone_lob="PL]"
//olone="Organ: Inflorescence at begining of development
(lone=long): Vector: pSport1; Site_1: Sal1; Site_2: Not1;
An unidirectional cDNA library generated from
[Inflorescence at begining of development (lcm-long)].
CDNA was prepared from polyA+ mRNA using SuperScript
Plasmid System Kit (Invitrogen). The double-strand cDNAs
were fractionated in a sepharose CL-2B 40cm-columns and
fragments sizing between 0.8 and 1.5 Kb were
directionally cloned into the vector. Details of each
source of RNA and library construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"
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Janear 2 to 787

Kudrna, D., Dean, R., Soder Jund, C., Wing, R. and Wang, G.

Large-scale identification of ESTs involved in the interaction
Detween rice and Magnaporthe grisea
Unpublished (2003)
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
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llarity 47.2%; Pred. No. 0.00011;
Conservative 0; Mismatches 191;
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Matches 171; Conserv
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Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E., Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G. Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea bit which shed (2003) Contact: Rod Wing Arizona Genomics Institute University of Arizona Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ BS721-0088, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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/note="Vector: pBluescript II KS +; Site 1: EcoRI; 
Xhol; 6 hrs after innoculation with Rice Blast (Che
86661)
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="txon:39947"
/clone="OSJNEA17P21"
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BACKWARD: aat taa ccc tca cta aag gg
Plate: 17 row: F column: 21
Seq primer: atc agc ggc cgc gat cc.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
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/dev_stage="3 week"
/dab_nost="DH108"
/clone lib="OSJNEC"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 6 hrs after innoculation with Rice_Blast (C9240-1)"
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Oryza sativa (japonica cultívar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
1 (bases 1 to 591)
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    .787
    /organism="Oryza sativa (japonica cultivar-group)"

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                                                                                                                                                                                                                                                     BACKWARD: gga aac agc tat gac cat g
Plate: 07 row: F column: 21
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
                                                                                 http://genome.arizona.edu
                                                                                                                                                                                                         FORWARD: gta aaa cga cgg cca gtg
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEC07F21"
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10.2%; Score 53.6; DB 6; I
44.5%; Pred. No. 0.00064;
ive 0; Mismatches 264;
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BACKWARD: gga aac agc tat gac cat g
Plate: 05 row: A column: 17
Seg primer: gta aaa cga cgg cca gtg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
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/cultivar="Nipponbare"
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clone="OSJNEc05A17"
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lab_host="DH108"
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EST.
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      EST 08-SEP-2004
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/tissue_type="Leaf"
/tissue_type="Leaf"
/dev_stage="one week"
/clone lib="Cold stressed rice cDNA library"
/note="Vector: pBluescript SK+; Cold treatment by placing at 4oC for 16 hour after growth on MS medium for one week"
                                                                                                                                           Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaae; Oryza.
1 (bases 1 to 665)
CV152413
LS245-S.SEQ Cold stressed rice cDNA library Oryza sativa (japonica cultivar-group) cDNA, mRNA sequence.
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Pred. No. 0.00063;
0; Mismatches 264; Indels
                                                                                                                                                                                                                                               Lee,J.-S.
Isolation and chromosomal mapping of the
induced under abiotic stress conditions
Unpublished (2004)
Contact: Lee Jung-Sook
                                                                                                                          Oryza sativa (japonica cultivar-group)
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/cultivar="Ilpumbyeo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: jungslee@rda.go.kr.
Location/Qualifiers
                                                                                  CV152413.1 GI:51946072
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ilarity 44.5%;
Conservative
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 698)
Jantasuriyarat,C., Lu,Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpubblished (2001)
Contact: Rod Wing EST 09-APR-2003 /clone lib="OSJNEC" /note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2: XhoI; 6 hrs after innoculation with Rice Blast (C9240-1)" ö 340 41 CGGCCGCCGCACTGGCGGAAGGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACACG 100 47 CAGCAGCGGCCATGGAGGGATACGACCGCGAGTTCTACCAGTCCCGCGACCAGCTGCGGC 106 101 CAAAAGCCTCAAGCTCTTTAGGTTCTGCCAAAGGCTTCAGCCCGCGCGTTCTCCGCAGGCT 160 107 TGCAGACGCGAGCTTCTCCGGCCTCTCCCTCGGCGACTCCATCTGGTCCTCCCCCCTCCG 166 161 ACCGCATCAACGACCTCCGCTTCGCCGTCGATTACACGCGCTACAAAAACTATAAAGCCC 220 226 221 CATCCACCGATTTCAAACTTTACAGCATCGGCGCGTCCGCCATTTACGACTTCGACACCC 280 227 CCAAGAACGCCATGGCCAACATCAACGGCGTCGCCGGAAACCTGGATGGCCCGGGCCTCA 286 287 TCGGCTCCGGCAAGCTCGCCTTCGGCGCCCAAGGCCGACCGCTACAACAGCGTCAACC 346 341 TGGGCGGCAGCGACAGCTTCAGCCAAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAA 400 CB653730 698 bp mRNA linear EST 09-APR-20 OSJNEC05A17.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA clone OSJNEC05A17 5', mRNA sequence. 281 AATCGCCCGTCAAACCGTATCTCGGCGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACT Arizona Genomics Institute University of Arizona Biological Sciences West, 448A, P.O. Box 210088, Tucson, Length 698 Indels

261

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/tissue_type="Seedling leaves"
/dev_stage="16-day-old rice seedling treated by JA/BTH"
/clone_lib="Subtracted cDNA library of JA/BTH-treated rice
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/cultivar="Drew (a major cultivated variety in Arkansas)"
/db xref="taxon:39947"
/clone="UB193"
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viidiplantae, Streptophyta, Embryophyta; Tracheophyta,
Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                          262 TCGGCTCCGGCAAGCTCGCCTTCGGCCCACCAAGGCCGACCGCTACAACAGCGTCAACC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                     341 TGGGCGGCAGCGACAGCTTCAGCCAAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAA 400
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         142 ACCGCCGCAACGAGCCGGCCTTCGACGGCGAGTACCACCACTTCTCCTCCCCCCTCCCCCG 201
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                                                                                                    221 CATCCACCGATTTCAAACTTTACAGCATCGGCGCGTCCGCCATTTACGACTTCGACACCC
                                                                                                                                                                                 281 AATCGCCCGTCAAACCGTATCTCGGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACT
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10.2%; Score 53.6; DB 7; Length 741;
Best Local Similarity 44.5%; Pred. No. 0.00064;
Matches 212; Conservative 0; Mismatches 264; Indels (
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217 Plant Sci Bldg, Fayetteville, AR 72701,
Tel: 501-575-5635
Fax: 501-575-7601
Email: yiyang@uark.edu
Seg primer: T7.
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Contact: Yinong Yang
Plant Pathology Department
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Speraryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryzaa.
Jabase; Dryzaae; Oryzaa.
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Largesecale identification of ESTs involved in the interaction
Unpublished (2003)
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/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
KhoI; 24 hrs after innoculation with Rice Blast (70-15)"
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347 TCCCGTCGACAACAACAACAAGACCAAGGCCGGCGGCGAAGATCAACAACA 406
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                                                                                                                                        401 GCTATGCCGTTACCCCGAATGTCGATTTGGATGCCGGCTACCGCTACAACTACATCGGCA 460
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/mol type="mRNA"
/cultivar="Nipponbare"
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University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson,
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Pred. No. 0.00064;
0; Mismatches 264; Indels
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BACKWARD: gga aac agc tat gac.cat g
Plate: 14 row: E column: 24
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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/clone="0SJNEe14224"
/tissue_type="leaf"
/dev stage="3 week"
/lab_host="DH108"
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Tel: 520 626 3967
Fax: 520 621 9288
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762 bp mRNA linear EST 09-APR-2003
Clone OSJNEe14C19 5', mRNA sequence.
CB677339
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Oryza sativa (japonica cultivar-group)
Bukaryota, Vizidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaa.
1 (Bases I to 762)
Jantasuriyarat, C., Lu, G. Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,
Rudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
                                  /note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2: XhoI; 24 hrs after innoculation with Rice Blast (70-15)"
                                                                                                                                                                                                                                                                                                                          CGGCCGCCGCACTGGCGGAAGGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACG 100
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Pred. No. 0.00065;
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University of Arizona
Biological Sciences West, 448A, P.O.
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Fax: 520 621 9288
Email: http://genome.arizona.edu
/clone_lib="OSJNEe"
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Jantascotter, 775, 200.
Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E., Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.
Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea
Unpublished (2003)
Arizona Genomics Institute
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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OSJNEe05117.f OSJNEe Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEe05117 5', mRNA sequence.
                                                                       CAAAAGCCTCAAGCTCTTTAGGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCT
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| organism="Oryza sativa (japonica cultivar-group)" | organism="Oryza sativa (japonica cultivar-group)" | organism="Nulpponbare" | orllivar="Nulpponbare" | db_xref="taxon:39947" | olone="OSJNBe05117" | olone="OSJNBe05117" | olone="OSJNBe05117" | olone="Asige="a week" | olone="DH108" | olone="DH108" | olone="Bh108" | olone="Asige="a week" | olone="Asige="a week" | olone="a week" | olon
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Biological Sciences West, 448A, P.O. Box 210088, Tucson,
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BACKWARD: gga aac agc tat gac cat g
Plate: 05 row: I column: 17
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Location/Qualifiers
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Tel: 520 626 3967
Fax: 520 621 9288
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59
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Oryza sativa (japonica cultivar-group)
    Arizona Genomics Institute
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                                                                         /mol_type="mRNA"

cultivar="Nipponbare"

db_xref="taxon:3947"

/cultivar="Nipponbare"

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/cultivar="taxon:3947"

/cultivar="taxon:3947"

/cultivar="taxon:3947"

/dev stage="Laaf"

/dev stage="1 week"

/dev stage="1 week"

/clone lib="OstNse"

/clone lib="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:

Xhol; 24 hrs after innoculation with Rice Blast (70-15)"
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Byermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Brhartoideae; Oryzeae; Oryza.
1 (bases I to 77)
Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,
Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.
Large-scale identification of ESTs involved in the interaction
Unpublished (2003)
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/organism="Oryza sativa (japonica cultivar-group)"
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                                                                                                                                                                                                                                                                                                                      10.2%; Score 53.6; DB 6; Length 762; ilarity 44.5%; Pred. No. 0.00065; Conservative 0; Mismatches 264; Indels
Seq primer: gta aaa cga cgg cca gtg.
Locat.on/Qualifiers
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OSJNECOTG20.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA clone OSJNECOTG20 5', mRNA sequence.
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/lab_host="DH108"
/clone_lib="0SUNBe"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
KhoI; 24 hrs after innoculation with Rice_Blast (70-15)"
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/mol_type="mRNA"
/cultivar="Nipponbare"
                                                                            ΑZ
University of Arizona
Biological Sciences West, 448A, P.O. Box 21008B, Tucson,
85721-008B, USA
Tel: 520 626 3967
Fax: 520 621 928B
Email: http://genome.arizona.edu
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FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 13 row: K column: 18
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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/clone="OSJNEe13K18"
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EST.
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280

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Oryza sativa (japonica cultivar-group)

ORGANISM

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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Coryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhatroideae; Oryzaee; Oryza.
I (bases 1 to 782)
Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E., Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.
Large-scale identification of ESTs involved in the interaction
Detween rice and Magnaporthe grisea
Unpublished (2003)
                                                                                          /ez bp mRNA linear EST 09-APR-2003 CSUNEGIIF07.f OSJNEG Oryza sativa (japonica cultivar-group) cDNA clone OSJNEGIIF07 5', mRNA sequence.
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XhoI; 24 hrs after innoculation with Rice Blast (C9240-I)"
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University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
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/organism="Oryza sativa (japonica cultivar-group)"
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Larity 44.5%; Pred. No. 0.00065;
Conservative 0; Mismatches 264; Indels
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BACKWARD: gga aac agc tat gac cat g
Plate: 11 row: F column: 07
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: http://genome.arizona.edu
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                                                                                                                                                                                                                                                                  CB665147.1 GI:29668872
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KEYWORDS
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Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
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Pred. No. 0.00065;
0; Mismatches 264; Indels
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BACKWARD: gga aac agc tat gac cat g
Plate: 07 row: G column: 20
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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Fax: 520 621 9288
Email: http://genome.arizona.edu
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/cultivar="Nipponbare"
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/clone="OSJNEc07G20"
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Best Local Similarity 44.5%;
Matches 212; Conservative
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Oryza sativa (japonica cultivar-group)
ENKARYOTA, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
ENKARYOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzeae; Oryza;
En (bases 1 to 561)
Kim,J.S., Jun,K.M., Cheong,Y.-W., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.-W., and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeongji, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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    281 AATCGCCCGTCAAACCGTATCTCGGCGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACT 340
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ive 0; Mismatches 261; Indels
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Location/Qualifiers
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/cullivar="Nackdong"
/cullivar="Nackdong"
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/clone="14ETL--04-H12"
/tissue_type="laaf"
/dev_stage="14 days after germination"
/lab_hoste="E_coli_DH108"
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Eukaryora, viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryora; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

Enthartoideae; Oryzeae; Oryza.

Enthartoideae; Oryzeae; Oryza.

Santaguriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E., Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G. Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea

Unpublished (2003)

Contact: Rod Wing

Arizona Genomics Institute
University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

Fax: 520 621 9288

Email: http://genome.arizona.edu
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/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 24 hrs after innoculation with Rice Blast (C9240-I)"
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                                                                                        338 TCCCCGTCGACAACAACAACAACAAGAGTCCTACGGCGGCGCCGCCAAGATCAACAACA
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/organism="Oryza sativa (japonica cultivar-group)"
/orlivar="MRNA"
/cultivar="Nipponbare"
/db xref="taxon:39947"
/clone="OSJNEG15K14"
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Pred. No. 0.00065;
0; Mismatches 264; Indels
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/dev_stage="3 week"
/lab_host="DH108"
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Matches 212; Conservative (
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ö 41 CGGCCGCCGCACTGGCGGAAGGCGCATCTGGTTTTACGTCCAAGCCGATGCCGCACACG 100 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR." Gaps

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71 CAGCAGCGGCCATGGAGGGATACGACCGCGAGTTCTACCAGTTCAGCGACCAGCTGCGGC 130
                                   101 CANANGCCTCANGCTCTTTAGGTTCTGCCANAGGCTTCAGCCCGCGCATCTCCGCAGGCT 160
                                                                  131 rechascosconderrereceserereteereseseneresereteereerese
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                                                                                                                                    221 CATCCACCGATTTCAAACTTTACAGCATCGGCGCGTCCGCCATTTACGACTTCGACACCC 280
                                                                                                                                                                                                         251 ccaagaaddccaardaccaacardaadggdgrddccggaaadcrggardgdccgggdcrda 310
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                                                                                                                                                                                                                                                                           311 TCGGCTCCGCCACGCCTTCGGCGCCCACGAGGCCGACCGCTACAACAGCGTCAACG 370
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Search completed: May 19, 2005, 19:31:26 Job time : 7711 secs

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Fri May
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version 5.1.6
- 2005 Compugen Ltd.
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      GenCore
Copyright (c) 1993
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May 19, 2005, 19:34:43 ; Search time 302 Seconds (without alignments) 222.835 Million cell updates/sec Run on:

US-10-650-123-2 868 Perfect score:

1 MKKALATLIALALPAALAE........VNTVKNVRSGELSVGVRVKF 174 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 Total number of hits satisfying chosen parameters:

2105692 segs, 386760381 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

A_Geneseq_16Dec04:* 1: geneseqp1980s:* 2: geneseqp1990s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2000s:* geneseqp2001s:* 8: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

, uo	Proteinas	N. mening	N. mening	Neisseria	Neisseria	N meningi	Neisseria	N meningi	Proteinas	Proteinas	Neisseria	Proteinas	N meningi	N. gonorr	N meningi	N meningi	Neisseria	Neisseria	N meningi	N meningi	N meningi	M catarrh	N. gonorr	Haemophi1	Haemophil
Description	Aaw04891	Abu79079	Adf43316	Ad116114	Ad113428	Ad124352	Adp08236	Ad124383	Aaw04893	Aaw04894	Abg91063	Aaw04892	Ad124385	Abp77991	Ad124387	Ad124386	Aab19895	Ad113426	Ad124384	Ad124388	Ad124389	Aao17579	Abp79561	Aau97605	Aau97603
ID	AAW04891	ABU79079	ADF43316	ADL16114	ADL13428	ADL24352	ADP08236	ADL24383	AAW04893	AAW04894	ABG91063	AAW04892	ADL24385	ABP77991	ADL24387	ADL24386	AAB19895	ADL13426	ADL24384	ADL24388	ADL24389	AA017579	ABP79561	AAU97605	AAU97603
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	5.5	5.5	5.2	5.1	14.7	4.7	4.4	24.2	3.9	13.7	3.6	22.4	22.4	50.5	6.2	9.6	5.3	5.2	4.6	4.1
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ALIGNMENTS

Proteinase K reistant; Neisseria meningitidis; Neisseria gonorrhoeae; Proteinase K resistant N. meningitidis 22 kD surface protein. antibody; detection; probe; surface protein. AAW04891 standard; protein; 174 AA. (revised)
(first entry) 16-OCT-2003 22-DEC-1996 AAW04891; RESULT 1 AAW04891

Neisseria meningitidis; strain 608B. 1. .19 /label= sig_peptide 20. .174 /label= mat_protein Location/Qualifiers Key Peptide Protein

WO9629412-A1.

26-SEP-1996

96WO-CA000157. 95US-00406362. 95US-0001983P. 15-MAR-1996; 17-MAR-1995;

(IAFB-) IAF BIO VAC INC.

04-AUG-1995;

Martin D, Hamel J, Rioux C; Brodeur BR,

WPI; 1996-443187/44. N-PSDB; AAT39039.

or Neisseria meningitidis antigen, highly conserved between different strains - useful for prodn. of antibodies for immunisation against, diagnosis of, N. meningitidis infection.

Claim 7; Fig 1; 117pp; English.

A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AAT39019) to AAT39040). The isolated 22 kD antigen, antigenic fragments of antibodies can be used in a vaccine for the prevention of infection by N. meningitidis or by N. gonorrhoeae in

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meningitidis infection. The antigen may also be used to detect antibodies specific to N. meningitidis antigen. DNA sequences encoding the antigen, or their fragments, can be used as probes for the detection of pathogenic Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                       FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 SQTSIGLGVLTGVSXAVTPNVDLDAGYRYNYIGKVNTVRNVRSGELSVGVRVKF 174
The antibodies may also be used diagnostically to detect N.
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                                                                                                                                                                          Length 174;
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meningitidis lipopolysaccharide protein. ABU79079 standard; protein; 174 AA (first entry) 18-JUN-2003 ABU79079; RESULT 2

Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis; gene therapy; mammalian cell receptor; cytostatic; tumour associated lipid; anergy; T cell; antigen presenting cell; APC; tumouricidal immunocyte; antitumour.

Neiserria meningitidis.

US2002177551-A1.

28-NOV-2002.

30-MAY-2001; 2001US-00870759

31-MAY-2000; 2000US-0208128P

(TERM/) TERMAN D S.

Terman DS;

WPI; 2003-361759/34.

N-PSDB; ACA64711

A mammalian cell receptor, useful in the treatment of cancer by binding to tumor associated lipids where the binding induces anergy or apoptosis T cells and antigen presenting cells.

Disclosure; Page; 167pp; English.

treatment of cancer, which binds to tumour associated lipids and induces anergy or apoptosis in the T cells and antigen presenting cells (APCs). Also included are a mammalian cell useful in the treatment of cancer where the receptor which binds tumour associated lipids and induces cellular inactivation or death is deleted or functionally deactivated, producing (MI) a tumouricidal immunocyte population in vivo in a mammal (by allowing tumour associated lipids to contact immunocytes in which receptors for immunosuppressive fatty acids, ceramides, glycolipids, sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides, The invention relates to a mammalian cell receptor, useful in the

Contect Aproximated approaches and proceedy. Totaling a superantigen (SAg) nucleotide inserted into a virus, a mammalian T cell useful in the treatment of cancer comprising a superantigen (SAg) nucleotide inserted into a virus, a mammalian T cell useful in the treatment of cancer (where an adaptor protein which inhibits T cell activation by tumour associated antigens is deleted or functionally deactivated) a composition useful in the treatment of cancer (comprising a lipid raft conjudated to a superantigen), producing allowing tumour associated lipids to contact immunocytes, in which receptors for the lipids are inactivated or deleted to produce a tumouricidal Apr contact Aprs, in which receptors for the tumour associated lipids to contact Aprs, in which receptors for the tumour associated lipids are transfirated or deleted to produce a tumouricidal y activated population ex vivo in a mammal (by allowing a tumour associated lipids are contact Aprs, in which receptors for the tumour associated lipids are daministering Aprs to the host), producing a tumour associated lipids to contact T cells, in which adaptor proteins, which inhibit T cell activated to produce a tumouricidal y activated or functionally deactivated to produce a tumouricidal population of T cells, and administering the tumouricidally activated T cells to the host). Contact T cells and administering the tumouricidally activated T cells to the host), cancer in a mammal (by administering a lipid in vivo), producing (MS) a tumouricidal T cell population in vivo in a mammal (by allowing a tumouricidal T cell population in vivo in a mammal (by allowing a tumouricidal T cell population in vivo in a mammal comprising allowing a tumouricidal T cell population in vivo in a mammal comprising allowing a cutoctionally deactivated or ontact immunocytes in vivo, The cutocrise which inhibit T cell activated or contact immunocytes in vivo at the cutouricidal antigen to contact immunocytes in vivo in a mammal contact immunocytes and cutocrise which inhibit T cell a proteoglycolipids are inactivated or tumours. Bacterial superantigens are co-administered or administered as fusion constructs with anti-tumour proteins or motifs. The present sequence represents an anti-tumour protein which is co-administered with was obtained in electronic format from the US patnet "seqdata.uspto.gov/sequence.html?DocID=20020177551" or incorporated into a fusion construct with a superantigen. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from the US patnet effice website at "sequata uspto.gov/sequence.html?DocID=20020177551" Sequence 174 AA;

;; Length 174; Indels Query Match 100.0%; Score 868; DB 6; Best Local Similarity 100.0%; Pred. No. 9.3e-87; Matches 174; Conservative 0; Mismatches 0;

Gaps

09 1 MKKALATLIALALPAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR

120 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 셤 ò ò

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ADF43316 standard; protein; 174 AA

ADF43316;

12-FEB-2004 (first entry)

N. meningitidis lipopolysaccharide seq id 36

receptor; lipid-based tumour associated antigen; cytostatic; antimicrobial; gene therapy; neoplastic disease; tumour; cancer; infectious disease; lipopolysaccharide; LPS.

RESULT 3

30-AUG-2002; 2002GB-00020194

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                                                                                                                                                                                                                                                                                  tumour (cancer), and infectious diseases. This is the amino acid sequence of Neisseria meningitidis lipopolysaccharide (LPS) to which tumour cells
                                                                                                                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                                                                                                            FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                                                                               The invention describes a receptor in a mammalian cell that inhibits regular activation by receptors specific for lipid-based tumour associated antigen. The receptor has cytostatic and antimicrobial properties and is suitable for use in gene therapy. The receptors, methods and compositions are useful for treating a neoplastic disease or
                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF
                                                                                                                                                                                                                                                                                                                                                                                     1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                    New receptor in a mammalian cell that inhibits regular activation by receptors specific for lipid-based tumor associated antigens, useful treating a neoplastic disease or tumor, and infectious diseases.
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                             100.0%; Score 868; DB 7; Length 174; 100.0%; Pred. No. 9.3e-87; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Outer membrane vesicle preparation, OMV, detergent-free, physical disruption; vaccine; serogroup B; NspA; Neisserial surface protein A; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neissería meningitidis NspA for use in vaccine.
                                                                                                                                                                                                            Disclosure; SEQ ID NO 36; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADL16114 standard; protein; 174 AA
                                                         28-DEC-2000; 2000US-00751708.
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                                                                              99US-0173371P.
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                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 174; Conservative
Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis
                                                                                                                                       WPI; 2003-787326/74.
N-PSDB; ADF43315.
                                                                                                (TERM/) TERMAN D S
                                                                                                                                                                                                                                                                                                       develop immunity.
                                                                                                                                                                                                                                                                                                                          Sequence 174 AA;
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                  US2003157113-A1
                                                                            28-DEC-1999;
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                                                                                                                    Terman DS;
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The invention relates to a process for producing an outer membrane vesicle (OWV) preparation from a bacterium. The process involves distrupting the bacterial membrane substantially in the absence of deoxycholate detergent or other detergent, followed by several centrifugation steps. Membrane disruption is achieveded by several homogenisation, microfluidisation, cavitation, osmotic shock, grinding, French press, belnding or any other physical technique. The outer membrane vesicles can be prepared from bacteria of the genera Moraxella, Shigella, Pseudomonas, Treponema, Porphyromonas, Helicobacter or Neisseria, and are particularly produced from Neisseria meningitidis especially serogroup B) or Neisseria genorrhoeae. The invention also relates to a Neisseria meningitidis outer membrane vesicle composition in which the vesicles include the immunogens NapA (Neisserial surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                 Producing an outer membrane vesicle (OMV) preparation from a bacterium, useful as a vaccine against Neisseria meningitidis serogroup B, comprises disrupting the bacterial membrane in the absence of deoxycholate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein A; ADL16114), 287 protein (ADL16113) and 741 protein (ADL16112); and the use of outer membrane vesicle compositions as a medicament, especially for raising an immune response in a patient. The method is useful for manufacturing an outer membrane vesicle preparation as a vaccine against Neisseria meningitidis serogroup B. The present sequence represents Neisseria meningitidis NspA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKFYLGARLSLNRASVDLGGSDSF
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100.0%; Score 868; DB 8;
Best Local Similarity 100.0%; Pred. No. 9.3e-87;
Matches 174; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 3; 20pp; English.
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                                                                                   Rappuoli
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                                                                                   Serruto D,
                                                                                                                                                              WPI; 2004-239124/22
(CHIR ) CHIRON SRL.
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                                                                                   Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
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The invention relates to an isolated reloided Neisserial surface procein alvention relates to an insolated reloided Neisserial surface procein in an alkalian also relates to the method of refolding an NspA protein; an alkalian erefolding buffer comprising ethanolamine and SB-12 (3-dimethyldodecylammoniopropanesulphoate) for refolding an NspA protein, a dimethyldodecylammoniopropanesulphoate) for refolding an NspA protein, a pharmaceutical composition comprising the refolded NspA protein, a carrier and optionally one or more other Neisserial antigens; a method of preventing or treating a Neisserial infection. NspA has constructeristics which indicate that it is a potential vaccine candidate for the development of subunit vaccines for the treatment of infections caused by Neisseria meningitidis (meningococcus), which causes invasive bacteraid diseases such as bacteraemia and meningitis, or Neisseria consorrhoeae, the causative agent of gonorrhoea. Recombinantly produced of NspA could therefore be used to produce vaccine compositions and it could also be used in the development of new antimircobial agents, diagnostic tests and in drug screening. However, recombinantly produced proteins are frequently unable to adopt their biologically active conformations, and yields may be very low due to mis-folding and aggregation of the protein. The method of the invention provides an improved method for refolding the possible to increase the recovery of active protein form partly purified inclusion bodies in amounts up to 100% without the need for further purification. The refolded NspA protein is useful for preparing a composition for diagnosing, treating or preventing infection caused by Neisseria meningitidis or Neisseria gonorrhoeae. The meningitidis H44/76.
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                                                                                                                                                                           /note= "The corresponding residue in the mature protein shown in Fig 2 (residue 149) is Ala"
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diagnosing, treating or preventing infection caused by Neisseria
meningitidis or Neisseria gonorrheae.
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1. 19
/label= Signal_peptide
20. 174
/label= Mature_NspA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLAXOSMITHKLINE BIOLOGICALS SA. RIJKSUNIV UTRECHT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Denoel P,
                                                                                                                                                                                                                                                                                                                                                                                                                        28-AUG-2003; 2003WO-EP010085
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Tommassen J, Weynants V;
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Matches 174; Conservative
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                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                   WO2004020452-A2.
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       Peptide
                                                                           Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition comprising liposome associated with isolated polypeptide or polynucleotide derived from Neisseria meningitidis strain 608B, or its fragment or analog, useful for inducing an immune response against N.
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                  121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
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121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
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100.0%; Pred. No. 9.3e-87;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                         NspA; vaccine; antibacterial; meningitis
                                                                                                                                                                                                                                     N meningitidis strain 608B NspA protein.
                                                                                                                           ADL24352 standard; protein; 174
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                                                                                                                                                                                                                                                                                                             Neisseria meningitidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Martin D, Rioux S;
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Best Local Similarity
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RESULT

us-10-650-123-2.rag

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Claim 9; SEQ ID NO 69; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      ADL24383 standard; protein; 174 AA.
                                                                                                        17-NOV-2003; 2003WO-IB006281
                                                                                                                   15-NOV-2002; 2002GB-00026734, 27-MAR-2003; 2003GB-00007131,
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.4%;
Matches 173; Conservative (
                                                                        Neisseria meningitidis MC58
                            26-AUG-2004 (first entry)
                                                                                                                                               Norais N, Grandi G,
                                                                                                                                                          WPI; 2004-420615/39.
                                                                                                                                    (CHIR ) CHIRON SRL.
                                                                                                                                                                                                                                                                        of the invention
                                                                                                                                                                                                                                                                                   Sequence 174 AA;
                                                                                   WO2004046177-A2
                                                                                              03-JUN-2004
                                                                                                                                                                                      infections
                 ADP08236;
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ADL24383
ID ADL2
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
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The present invention relates to a pharmaceutical composition comprising a liposome associated with an isolated polypeptide derived from Neisseria meningitidis strain 608B, where the polypeptide is the NBA protein. The composition is useful for inducing an immune response against N. meningitidis, for preventing and/or treating N. meningitidis infection and for treating and/or preventing neisserial infection chosen from N. meningitidis, N. gonorrhoeae, N. lactamica and N. polysaccharea. It is useful for treatment or prophlylaxis of meningitis and meningoccaemia, in a host. The host is a mammal, preferably a human and more preferably an adult human. The present sequence is a modified version of the Neisseria meningitidis strain 608B NSpA protein. Note: This sequence is not shown in the specification but has been created based on the information given and the wild-type NSpA protein shown in Figure 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Composition comprising liposome associated with isolated polypeptide or polymucleotide derived from Neisseria meningitidis strain 608B, or its fragment or analog, useful for inducing an immune response against N. meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKKALATLIALALPAPAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 174;
                                                                                                                                                                                                                                                                                                            /note= "wild-type Gly substituted by Ala"
                                                                                                                                                                                                                                                                                                                                                              /note= "wild-type Asp substituted by Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                         mutein; mutant; NspA; vaccine; antibacterial; meningitis.
                                                                                          N meningitidis strain 608B modified NspA protein #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 857; DB 8;
Pred. No. 1.5e-85;
1; Mismatches 1
                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Page; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-AUG-2003; 2003WO-CA001452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-AUG-2002; 2002US-0406980P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.7%;
                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SHIR-) SHIRE BIOCHEM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 98.7
Best Local Similarity 98.9
Matches 172; Conservative
                                                                                                                                                                                         Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-239123/22.
                                                                                                                                                                                                                                                                                     Misc-difference 115
                                                                                                                                                                                                                                                                                                                                       Misc-difference 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Martin D, Rioux S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             WO2004019976-A2
                                             03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAR-2004
                                                                                                                                                                                                               Synthetic.
ADL24383;
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ል<sup>:</sup> አ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel composition comprising outer-membrane vesicles (OWV) prepared from a first strain of Neisseria meningitidis and 1 or more proteins which are present in OWVs prepared from a second strain of N. meningitidis, but which are not present in OWVs prepared from the first strain. The composition of the invention demonstrates antibacterial and antihilammatory activities and may be useful in the field of meningococcal biochemistry, in particular the trafficking and localisation of meningococcal infections, as well as in the prevention or treatment of meningococcal infections, possibly via the production of a vaccine or gene therapy. The current sequence is that of a Neisseria meningitidis MCSB outer-membrane vesicle (OWV)-related membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New compositions having outer-membrane vesicles and proteins from Neisseria meningitidis, useful in the field of meningococcal blochemistry, in particular for preventing and/or treating meningococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
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                                                                                                                                                             Neisseria meningitidis MC58 OMV-related membrane protein - SEQ ID 69
                                                                                                                                                                                                     outer-membrane vesicle; antibacterial; antiinflammatory;
meningococcal protein trafficking; localisation; infection; vaccine;
gene therapy.
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Pred. No. 2.5e-86;
0; Mismatches 1; Indels
                 ADP08236 standard; protein; 174 AA.
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9 9 120

121

RESULT 9 AAW04893

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AAW04894 standard; protein; 174 AA.
                                                                                                                                                                                                                          WO9629412-A1
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                                                                                                                                                                                                                                                                                            17-MAR-1995;
04-AUG-1995;
                                           16-OCT-2003
22-DEC-1996
                                                                                                                                                                                                                                                                                                                             (IAFB-) IAF
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                      AAW04894;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis antigen, highly conserved between different strains - useful for prodn. of antibodies for immunisation against, or diagnosis of, N. meningitidis infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                 Proteinase K reistant; Neisseria meningitidis; Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
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                                                                             Proteinase K resistant N. meningitidis 22 kD surface protein.
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                                                                                                                                                                                                                                                                                                                                                    Rioux C;
                                                                                                                                                                   1. 19
/label= sig_peptide
20. 174
/label= mat_protein
                                                                                                                                   Neisseria meningitidis; strain Z4063
                                                                                                                                                          Location/Qualifiers
 AAW04893 standard; protein; 174 AA.
                                                                                                                                                                                                                                                                                                                                                    Hamel J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Fig 9; 117pp; English.
                                                                                                                                                                                                                                                                       96WO-CA000157
                                                                                                                                                                                                                                                                                            95US-00406362
95US-0001983P
                                                        (first entry)
                                                                                                                                                                                                                                                                                                                             (IAFB-) IAF BIO VAC INC
                                                                                                                                                                                                                                                                                                                                                    Martin D,
                                             (revised)
                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-443187/44.
N-PSDB; AAT39041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 174 AA;
                                                                                                                                                                                                                                                                       15-MAR-1996;
                                                                                                                                                                                                                                                                                            17-MAR-1995;
04-AUG-1995;
                                                                                                                                                                                                                            WO9629412-A1
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                                            16-OCT-2003
                                                      22-DEC-1996
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                      AAW04893;
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A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AAT33039 to AAT39042). The isolated 22 kD antigen, antigent fragments of antibodies can be used in a vaccine for the prevention of infection by N. meningitidis or by N. gonorrhoeae in humans. The antibodies may also be used diagnostically to detect N. meningitidis infection. The antigen may also be used to detect antibodies specific to N. meningitidis antigen may so be used to detect antibodies or their fragments, can be used as probes for the detection of pathogenic Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
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                                                                                                                                        Proteinase K reistant; Neisseria meningitidis; Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
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strains - useful for prodn. of antibodies for immunisation against,
diagnosis of, N. meningitidis infection.
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                                                                                       Proteinase K resistant N. meningitidis 22 kD surface protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rioux C;
                                                                                                                                                                                                                                                                                                                                                1. .19
/label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                 20. .174
/label= mat_protein
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                               Neisseria meningitidis; strain b2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Martin D, Hamel J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Fig 10; 117pp; English.
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                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIO VAC INC.
(revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-443187/44.
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RESULT 11 ABG91063

RESULT 10 AAW04894

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A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AAT39939 to AAT39042). The isolated 22 kD antigen, antigenic fragments of antibodises can be used in a vaccine for the prevention of infection by N. meningitidis or by N. genorrhoeae in humans. The antibodies may also be used diagnostically to detect N. meningitidis infection. The antigen may also be used to detect antibodies specific to N. meningitidis antigen. DNA sequences encoding the antigen, or their fragments, can be used as probes for the detection of pathogenic Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis antigen, highly conserved between different
strains - useful for prodn. of antibodies for immunisation against,
diagnosis of, N. meningitidis infection.
  antibody; detection; probe; surface protein.
                                                                                                                                                                                                                                                                                               Hamel J, Rioux C;
                              meningitidis; strain MCH88
                                                                                               20. .175
/label= mat_protein
                                                                        1. .19
/label= sig_peptide
                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Fig 8; 117pp; English.
                                                                                                                                                                                                96WO-CA000157.
                                                                                                                                                                                                                          95US-00406362.
95US-0001983P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                               Martin D,
                                                                                                                                                                                                                                                                    IAFB-) IAF BIO VAC
                                                                                                                                                                                                                                                                                                                           WPI; 1996-443187/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAT39040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 175 AA;
                                                                                                                                         WO9629412-A1
                                                                                                                                                                                                15-MAR-1996;
                                                                                                                                                                                                                                        04-AUG-1995;
                                                                                                                                                                                                                                                                                               Brodeur BR,
                                                                                                                                                                                                                          17-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUN-2004
                                                                                                                                                                    26-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167;
                              Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Si
Matches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADL24385;
                                                         Key
Peptide
                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADL24385
ID ADL2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a new gram-negative bacterial bleb presenting on its surface the PorB outer membrane protein from Chlamydia trachlomatis, or a protective antigen from C. pneumoniae. The invention is useful for preventing C. trachomatis or C. pneumoniae infection in a host. The present amino acid sequence represents a Neisseria gonorrhoeae protein as described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                                                                                                                     Novel gram-negative bacterial bleb presenting on its surface PorB outer membrane protein from Chlamydia trachomatis or protective antigen from Chlamydia pneumoniae, useful for preventing Chlamydia infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proteinase K reistant; Neisseria meningitidis; Neisseria gonorrhoeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                           Gram-negative bacterial bleb; PorB; outer membrane protein;
Chlamydia trachomatis infection; Chlamydia pneumoniae infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteinase K resistant N. meningitidis 22 kD surface protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
                                                                                                                                                                                                                                                                                                                                      Poolman J, Verlant VGCL;
                                                                                 Neisseria gonorrhoeae outer membrane protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 825; DB 5;
Pred. No. 4.8e-82;
2; Mismatches 8
                                                                                                                                        protective antigen; antibacterial; vaccine.
                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
 standard; protein; 174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 54; 75pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW04892 standard; protein; 175 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%;
                                                                                                                                                                                                                                                    08-FEB-2002; 2002WO-EP001356.
                                                                                                                                                                                                                                                                                08-FEB-2001; 2001GB-00003169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                      (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                      Berthet FJ, Lobet Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
                                                                                                                                                                   Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-657510/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABS67381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 174 AA;
                                                                                                                                                                                             WO200262380-A2
                                                     29-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2003
22-DEC-1996
                                                                                                                                                                                                                         15-AUG-2002
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                           ABG91063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local ?
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IID AAW0
XX
AC AAW0
XX
DT 16-C
DT 22-D
XX
XX
XX
DE Prot
XX
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                                                                                                                                             1 MKKALAALIALALPAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                   FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS
                                                                                                                                                                                                                                              FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSDS
                                                                                                 1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                     Gaps
                                                                                                                                                                                                                                                                                                                           FSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                1,
  DB 2; Length 175;
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mutein; mutant; NspA; vaccine; antibacterial; meningitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N meningitidis strain 608B modified NspA protein #3
Score 824.5; DB 2
Pred. No. 5.5e-82;
0; Mismatches 7
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                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a pharmaceutical composition comprising. a liposome associated with an isolated polypeptide derived from Neisseria meningitidis strain 608B, where the polypeptide is the NspA protein. The composition is useful for inducing an immune response against N. meningitidis, for preventing and/or treating N. meningitidis infection meningitidis, N. gonorrhoeae, N. lactamica and N. polysaccharea. It is useful for treatment or prophylaxis of meningitis and meningoccaemia, in a host. The host is a mammal, preferably a human and more preferably an adult human. The present sequence is a modified version of the Neisseria meningitidis strain 608B NspA protein. Note: This sequence is not shown in the specification but has been created based on the information given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52
                                                                                                                                                                                                                                                                        Composition comprising liposome associated with isolated polypeptide or polynucleotide derived from Neisseria meningitidis strain 608B, or its fragment or analog, useful for inducing an immune response against N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKKALATLIALALPAAALAEGASGFYVQADAAHAK-----KGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKANVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
8
                                    Key Location/Qualifiers
Misc-difference 35. .36
/note= "wild-type NspA residues 36-43 deleted"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.5%; Score 820; DB 8; Length 166; 95.4%; Pred. No. 1.6e-81; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and the wild-type NspA protein shown in Figure 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibacterial; infection; vaccine; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N. gonorrhoeae amino acid sequence SEQ ID 2512.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP77991 standard; protein; 175 AA
                                                                                                                                                                                                                                                                                                                                        Example 4; Page; 79pp; English.
                                                                                                                                           29-AUG-2003; 2003WO-CA001452
                                                                                                                                                                    30-AUG-2002; 2002US-0406980P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry
                                                                                                                                                                                              (SHIR-) SHIRE BIOCHEM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 95.4
Matches 166; Conservative
Neisseria meningitidis
                                                                                                                                                                                                                                               WPI; 2004-239123/22
                                                                                                                                                                                                                        Rioux S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 166 AA;
                                                                                         WO2004019976-A2
                                                                                                                                                                                                                                                                                                             meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAR-2003
                                                                                                                                                                                                                        Martin D,
              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
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120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKKALAALIALAAAALAEGASGFYVQADAAHAKASSSLGSAKGFSFRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                        New protein from Neisseria gonorrheae, useful for the manufacture of medicament for treating or preventing N. gonorrheae infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 FSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 151. .152
/note= "wild-type NspA residues 152-163 deleted"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6; Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutein; mutant; NspA; vaccine; antibacterial; meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N meningitidis strain 608B modified NspA protein #5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 93.1%; Pred. No. 2.5e-80;
Matches 163; Conservative 2; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 371; 815pp; English
                                                                                                                                                                                                                                                Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADL24387 standard; protein; 162 AA
                                                                                                                         12-FEB-2002; 2002WO-IB002069.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis.
Neisseria gonorrhoeae.
                                                                                                                                                                                                                                                     Pizza M,
                                                                                                                                                                                                                                                                                             WPI; 2003-058415/05.
                                                                                                                                                                                                             (CHIR-) CHIRON SPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 175 AA;
                                                                                                                                                                                                                                                                                                                   N-PSDB; ABZ38961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004019976-A2
                                       WO200279243-A2
                                                                                                                                                                                                                                                       Fontana MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JUN-2004
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                                                                               10-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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us-10-650-123-2.rag

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29-AUG-2003; 2003WO-CA001452.
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(SHIR-) SHIRE BIOCHEM INC.

30-AUG-2002; 2002US-0406980P.

Martin D, Rioux S;

WPI; 2004-239123/22.

Composition comprising liposome associated with isolated polypeptide or polymorcleotide derived from Neisseria meningitidis strain 608B, or its fragment or analog, useful for inducing an immune response against N. meningitidis.

Example 4; Page; 79pp; English.

The present invention relates to a pharmaceutical composition comprising a liposome associated with an isolated polypeptide derived from Neisseria meningitidis strain 608B, where the polypeptide is the Nmph protein. The composition is useful for inducing an immune response against N. meningitidis, for preventing and/or treating N. meningitidis infection and for treating and/or treating neisserial infection chosen from N. meningitidis, N. gonorrhoeae, N. lactamica and N. polysaccharea. It is useful for treatment or prophylaxis of meningitis and meningoccaemia, in a host. The host is a mammal, preferably a human and more preferably an adult human. The present sequence is a modified version of the Neisseria meningitidis strain 608B NspA protein. Note: This sequence is not shown in the specification but has been created based on the information given and the wild-type NspA protein shown in Figure 1.

Sequence 162 AA;

Query Match 91.5%; Score 794; DB 8; Length 162; Best Local Similarity 93.1%; Pred. No. 1.1e-78; Matches 162; Conservative 0; Mismatches 0; Indels 12; Gaps

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PAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120

61

61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174 121 요

Search completed: May 19, 2005, 20:55:00 Job time : 304 secs

121

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149, App 57, Appl 12284, A 5331, Ap 5, Appli 5146, Ap 30094, A 7781, Ap

Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Scoring table:

Searched:

Database

Perfect score: Sequence:

OM protein

Run on:

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RESULT 1

US-08-913-362-2

US-08-913-362-2

Sequence 2, Application US/08913362

Patent No. 6287574

GENERAL INFORMATION:

APPLICANT: Bardeur, Bernard R

APPLICANT: Hamel, Josee

APPLICANT: Hamel, Josee

APPLICANT: Hamel, Josee

APPLICANT: RABORTION: PROTEINASE K RESISTANT SURFACE PROTEIN

TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS: 30

CORRESPONDENCE ADDRESS: 30

CONFUTRY: USA

ZITY: Washington

STATE: D.C.

COUNTRY: USA

ZITY: READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: EMPORATION: MSELease #1.0, Version #1.30

SUFTARE: PATOR DATA: WORLS: US/08/913,362

PILING DATE: 13-NOV-1997

PRIOR APPLICATION DATA: WORLS: US/08/913,362

PRIOR APPLICATION NUMBER: US 08/406,362

PRIOR APPLICATION NUMBER: US 08/406,362
                                                                            US-09-069-584-57
US-09-902-540-12284
US-09-322-5331
PCT-US55-13749-5
US-09-328-352-5346
US-09-328-352-5146
US-09-328-352-781
US-09-418-980-8
US-09-902-540-14682
US-09-902-540-14682
US-09-902-540-14682
US-09-902-540-14682
US-09-903-544-56
US-09-69-236-2676
US-09-69-236-2676
                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : (202) 672-5300
(202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein US-08-913-362-2
85.5
85.5
85
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Sequence 2, Appli
Sequence 6, Appli
Sequence 9, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 2245, Ap
Sequence 7245, Ap
Sequence 7922, Ap
Sequence 7922, Ap
Sequence 7929, A
Sequence 7929, A
Sequence 7929, A
Sequence 7929, A
Sequence 7929, Ap
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Sequence 2, Appli
Sequence 1, Appli
Sequence 16267, A
Sequence 11, Appl
                                                                                                                                            May 19, 2005, 20:41:43; Search time 113 Seconds (without alignments) 114.946 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                               1 MKKALATLIALALPAALAE.........VNTVKNVRSGELSVGVRVKF 174
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Sequence 7,
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(Ggn2_6/ptodata/1/iaa/5A_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/5B_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/6A_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/6B_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-913-362-8

US-08-913-362-8

US-08-913-362-8

US-08-913-362-4

US-08-913-362-4

US-08-913-362-26

US-08-913-362-26

US-09-540-238-226-26

US-09-540-238-236-24

US-09-540-238-20

US-09-543-681A-7922

US-09-543-681A-7922

US-09-543-681A-7922

US-09-543-681A-7922

US-09-543-681A-7923

US-09-543-681A-7923

US-09-543-681A-751

US-09-164-714-7

US-09-164-714-7

US-09-164-714-7

US-09-952-267B-3

US-08-457-997B-2

US-08-457-997B-2

US-08-451-184-2
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JS-09-336-447A-11
JS-09-952-267B-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                         513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                    US-10-650-123-2
868
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Match Length
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854 838.5 824.5 135 135 113.5 100.5 104.5 92.5 89.5 88.5 88.5

Score

Result

DB 3; Length 174;

us-10-650-123-2.rai

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                                                                                                                                                61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                          61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT:
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Hamel, Josee
APPLICANT: Hamel, Josee
APPLICANT: Hamel, Josee
APPLICANT: OF INVENTION: Clement
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.4%; Score 854; DB 3; Length 174; 98.3%; Pred. No. 3.4e-91; ive 0; Mismatches 3; Indels
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 2007-5109
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRICK APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-NAR-1995
RILING DATE: 17-NAR-1995
FILING DATE: 04-AUG-1995
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Benc, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELEFPHONE: (202)672-5300
100.0%; Pred. No. 7.9e-93; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08913362
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TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
Best Local Similarity 100.
Matches 174; Conservative
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Best Local Similarity 98.3
Matches 171; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & L
STREET: 3000 K Stree
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US-08-913-362-6
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61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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                                                                                                          121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                   121 SQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174
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                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATPONREY/AGENT INPOMMATION:
NAME: BEHC, Stephen A:
REGISTRATION NUMBER: 29,768
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Patent No. 6287574
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TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
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COUNTRY: USA
7TP: 20007-5109
"TP: PRADBLE FT
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
121 FSQTSXGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
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0
                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 825; DB 3; Length 174;
Pred. No. 7.9e-88;
2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER SEADABLE FORM:
MEDIUM TYPE: F10.ppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: F10.ppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: US 60/001,983
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAMME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        3000 K Street, N.W., Suite 500
                                                                                                        Sequence 8, Application US/08913362
Patent No. 6287574
                                                                                                                                                                                                                                                                                                                                                      Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 94.3%;
Matches 164; Conservative
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INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (202) 672-5300
(202) 672-5399
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                                                                                                                                                                                                                                                                                                                                                          ADDATEST: 3000
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3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           relephone:
                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-913-362-8
                                                                                        US-08-913-362-8
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Sequence 4, Application US/08913362 Patent No. 6287574

RESULT 5 US-08-913-362-4

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61 FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSDS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MXKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 FSQTSTGLGVLAGVSYAVIPNVDLDAGYRYNXIGKVNTVKAVRSGELSAGVRVKF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
CORRESPONDENCE: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3; Length 175;
                 APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
TUTNER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: US 60/001,983
FILING DATE: O4-NuG-1995
ATTORNEY/AGBWT INFORMATION:
NAME: Bent, Stephen A.

REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 20,768
REFERENCE/DOCKET NUMBER: 20,768
REFERENCE/DOCKET NUMBER: 20,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 95.0%; Score 824.5; DB 3; Best Local Similarity 95.4%; Pred. No. 9.1e-88; Matches 167; Conservative 0; Mismatches 7;
                                                                                                                                       STREET: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 2000-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk .
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/08127499A Patent No. 5510264 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
     Martin, Denis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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APPLICANT:
APPLICANT:
APPLICANT:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTONEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 26.3%
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             unknown
    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-482-847-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-08-913-362-26
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Sequence 20, Application US/08482847

Batent No. 5556757

GENERAL INFORMATION:

APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARNA, Lawrence Rajendra
APPLICANT: SHARNA, Lawrence Rajendra
TITLE OF INVENTION: BACTERIAL.AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLGY & Lardner
STREET: 3000 & Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 IHPRVSVGYDFGGWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48;
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                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT: Stephen A.
REGISTRATION NUMBER: 59,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
SELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 LYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.6%; Score 135; DB 26.3%; Pred. No. 1.3e tive 20; Mismatches
                      *3000 K Street, N.W., Suite 500 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 ATLIALALPAALAEGASGFYVQADAAH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 FSPRISAGYRINDLRFAVDYTRYKNY----
                                                                                                             ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 26.3
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: unknown US-08-127-499A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
US-08-482-847-20
                                                                                              COUNTRY:
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75 IHPRVSVGYDFGGWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHA 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26, Application US/08913362
Fatent No. 6287574
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
APPLICANT: Hamel, Josee
APPLICANT: Hamel, Josee
APPLICANT: ROUX, Clement
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
MUMBER OF SEQUENCES: 30
CORRESPONDENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                              Length 170;
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MEDIUM TYPE: RIOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTONNEY/AGENT INPORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 LYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD 113
                                                                                                                                                                                                                                                                                                                                                                   15.6%; Score 135; DB 1; 26.3%; Pred. No. 1.3e-07; Live 20; Mismatches 47;
**REFERENCE/DOCKET NUMBER: 29,768

**REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
TELERA: 904136

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TTRANDENNES:
STRANDENNES:
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Sequence 7922, Application US/09543681A

Sequence 7922, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:

APPLICATION:

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

TITLE REFERENCE: 2709.1002-001

CURRENT PAPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR PAPLICATION NUMBER: US 60/128,706

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 7922

LENGTH: 384
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APPLICANT: GARY BRETON:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI
TITLE OF INVENTION: UDAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US 40/9/543, 681A
PRIOR APPLICATION NUMBER: US 60/128,706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 KPY--LGARL-----SLNRASVDLGGSDSFSQTSIGLGVL--TGVSYAVTPNVDLDAG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 DVYTRLGGMVWRADSTATINATSA--GTOKRFSENDTGVSPVFALGTEYAITPNIATRLE 197
                                                                                                                                                                                                                                     100 YLGARLSLNRASVDLGGSDSFSQTSIGLGV-----LTGVSYAVTPNVDLDAGYRY-NYI 152
                                                                                                          64
                                                                                                                                                   45 -GFSPRISAGYRINDLRFAVDYTRYKNYKAPSTDFKLYSIGASAIY----DFDTOSPVKP 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 MKK---TAIALAVAVAAFATAAQAAPKDNTWYTGGKLGWSQYQSTGNNWDGVNIGNGSTH 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 SPRIS----AGYRIND---LRFAVDYTRYKNYKAPSTD--FKLYSIGASAIYDFDTQSPV 97
                                                                                            1 MKKALATLIALALPAALAEGASG-----FYVQADAAHAKASS-----SLGSAKGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43; Gaps
                            Gaps
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                                                                    1 MKKALATLIA--LALPAALAEGASGFYVQADAAHAKASSSLGSAK--
      25.2%; Pred. No. 0.00014; ive 26; Mismatches 78; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 YRY-NYIGKVNTVKNVR--SGELSVGVRVKF 174
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Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                   166 GKDGNRDNTLADGAYAGVNFRF 187
                                                                                                                                                                                             65 DGDSVGLGMGYNFNLGPF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 26.1.
Best Local Similarity 26.1.
                          51; Conservative
Best Local Similarity
Matches 51; Conserve
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US-09-543-681A-7922
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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13699, Application US/09489039A

Patent No. 6610836
GENERAL INFORMATION
BATTLE OF INVENTION: WICLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: WREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 98;
                                                                                                                                                                                                                                                                                                                                           15.3%; Score 133; DB 3; Length 25; 100.0%; Pred. No. 1.3e-08; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 113.5; DB 4
Pred. No. 1.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.6%; Score 109.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2245
LENGTH: 98
    047998/0128
                                                                                                                                                                                                                                                                                                                                                                                                                                 61 FAVDYTRYKNYKAPSTDFKLYSIGA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FAVDYTRYKNYKAPSTDFKLYSIGA 25
                                                                                                                                                                                                                                                       ORGANISM: Neisseria meningitidis
STRAIN: 608B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2245, Application US/09540236 Patent No. 6673910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13699
  REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-530
TELEFAX: (202) 672-539
                                                                                   TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Watches 25; Conservative
                                                                                                                                                   25 amino acids
                                                                                                                                                                                                               MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: M.catarrhalis
US-09-540-236-2245
                                                                                                                                                                          amino acid
                                                                                                                                                                                             linear
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                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                               LENGTH:
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US-09-489-039A-7451
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  US-09-540-236-2792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 HGQMEVALINNFSYN-GKENQQSKSAFAYG--AGIQFNPYPNIAIDASYEYT---KLDAFK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 KALKTLFIATALLGSAAGVQAADNPV--GLTWGETSNNIQKSKSLNRNLNSPNLDKVIDN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TGTWGIRAGQQFEQGRY---YATYENISDTSSGNKLRQ--QNLLGSYDAFLPIGDNNTKL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 YLGARLSLNRASVDLGGSDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRY----- 149
                                                                                                                                                                                                                                                                                                                                            57 N-DLRFAV------DYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGA- 103
                                                                                                                                                                                                                                                                                                                                                                    66 EFDNQWGMIGSFVYTHQGYDY-HWNSRKIGSIDLDYYSLAAGPVYRFNDYISAYGLVGVA 124
                                                                                                                                                                                                                                                                                                                                                                                                                             ----RLSLNRASVDLGGSDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVK 159
                                                                                                                                                                                                                                                                                     ----ISAGYRINDLRFAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPV----KP
                                                                                                                                                                                                                                                        2 KKALATLI--ALALPAA-ALAEGASGFYVQADAAHAKASSS--LGSAKGFSPRISAGYRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 KALATL-IALALPAALAEGASGFYVQADAAHAKASSSLGSAKGF----SPR-----
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                                                                                                                                                                     Score 93; DB 4; Length 190;
Pred. No. 0.012;
                                                                                                                                                                                                            , 16;
                                                                                                                                                                  Query Match
10.7%; Score 93; DB
Best Local Similarity 26.0%; Pred. No. 0.01:
Matches 50; Conservative 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 PHGGNKLGSLDLHS---SSQFYLGANYKF 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----NYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19759, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7684
LENGTH: 190
                                                                                   ; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 -VGTWMLGLGYR 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 NVRSGELSVGVR 171
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Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-09-252-991A-19759
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RESULT 14

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Sequence 2792, Application US/09540236

Sequence 2792, Application US/09540236

Patent No. 6673910

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
APPLICANT: SOUSTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001

CURRENT PELING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 2792

FENCH A DESCRIPTION OF SEQ ID NOS: 3840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7451, Application US/09489039A

Factor No. 6610836

GENERAL INFORMATION:

APPLICANT: GATY Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 1999-01-27

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 7451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 GYRINDLRFAVDY----TRYKNYKAPSTDFK--LYSIGASAIYDFD-TQSPVKPYLGARL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 GYNF-DQNFGVEABFVGSDAKEFNAGMSPVKGDVKSFGAYGTYRYNFINTPF--YAKGKL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 SLNRASVDLGG-----SDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 RFAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLN-----RASV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----SDSFSQTSIGLG 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKK-ALATLIALALPAAALAEGASGFYVOADAAHAKASSSLGSAKGFSPRISAGYRINDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.3%; Score 89.5; DB 26.7%; Pred. No. 0.03; tive 29; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 -- DANAISLGTHLAF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 26.7%
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    ), ORGANISM: M.catarrhalis
US-09-540-236-2792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 D-----
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Search completed: May 19, 2005, 21:04:18 Job time : 113 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

May 19, 2005, 20:34:09 ; Search time 69 Seconds (without alignments) 242.634 Million cell updates/sec

US-10-650-123-2 868 I MKKALATLIALALPAAALAE......VNTVKNVRSGELSVGVRVKF 174 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seg length: 0 Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Description	outer membrane pro	outer membrane pro	protein	protein	>	y protein	y protein	y protein	y protein	y protein	y protein-	>	protein	y protein	opacity protein op	protein	opacity protein op	protein	>	y protein	protein	>	protein		protein	protein	y protein	protein	>
	QI	11,	B81932	S16610	S16611	S16613	S16612	KONH0	836343	S16614	S16616	S08514	S20043	S04380	KONH2C	S72343	S36329	S16617	S36342	S36341	836350	KONH8	S36348	836349	4-4	S36346	PL0038	36	641	S28630
	8	7	7	N	N	7	~	~4	7	N	N	~	~	~	-	7	~	~	~	~	N	Н	~	~	~	~	~	~	~	7
	Length	174	174	261	260	338	258	260	237	257	266	258	254	270	268	283	234	282	234	234	233	234	234	238	261	243	248	238	178	239
,	Match	6	98.4	28.2	-	۲.	7	27.8	7	27.7	27.5	27.4	27.3	27.3	27.2	7	26.8	ġ	26.7	Ġ	Ġ	ė	Ġ	•	Ġ	'n	'n	25.2	<u>.</u> .	24.8
	Score	864	854	244.5	4	241.5	241	241	240.5	5	239	238	237	237	236.5	N	232.5	32	232	232	231	226	226	226	226	224.5	221	219	217	215
1,000	No.	7	~	m	4	S	9	7	80	σ	10	11	12	13	14	15	16		18	19	20	21	22	23	24	25	56	27	28	53

RESULT 2

outer membrane protein NMA0862 [imported] - Neisseria meningitidis (strain 22491 serogrou cuter membrane protein NMA0862 [imported] - Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: B81932
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell
A;Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: B81932
A;Status: preliminary

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\$28627 \$44706 \$44707 \$44707 \$164187 \$20044 \$10256 \$10256 \$10266 \$16286 \$16286	A63556 I54668
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247 235 235 235 1121 1168 1170 239 281 201 201	784 784
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205.5 203.5 189.5 180.5 180.5 141 135 129.5 126.5 126.5	121.5
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	4 4

ALIGNMENTS

RESULT 1 G81174 outer membrane protein NsgA NMB0663 [imported] - Neisseria meningitidis (strain MC58 serc C;Species: Neisseria meningitidis
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_cnange 09-uur-2004 C;Accession: G81174
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
 A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, B.R.; Rappuoli, R.; Ver
 A;Title: Complete genome sequence ot Neisseria meningitidis serogroup B strain MC58. A;Reference number: A81000; MUID:20175755; PMID:10710307
A, Accession: G81174
A;Status: preliminary A:Molecule type: DNA
 A; Residues: 1-174 <tet></tet>
A;Cross-references: UNIPROT:Q9RP17; GB:AE002420; GB:AE002098; NID:g7225876; PIDN:AAF41081 A:Experimental source: serogroup B, strain MC58
Query Match 99.5%; Score 864; DB 2; Length 174; Rest Loral Similarity 99.4%; Pred No. 1.46-69;
vative 0
Qy 1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
 Db 1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
 Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKFYLGARLSLARASVDLGGSDSF 120
 Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
 Qy 121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKAVRSGELSVGVRVKF 174
 Db 121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174

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257

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C;Date: 04-Jun-1997 #sequence revision 17-Oct-1997 #text_change 09-Jul-2004
C;Accession: S16611; S36345; $28624
R;Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, I Mol. Microbiol. 5, 1889-1901, 1991
A;Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a famil A;Reference number: S16610; MUID:92114767; PMID:1815562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A/Cross-references: UNITROT: 004882; EMBL:X52371
A/Experimental source: strain MS11, variant 4.8
A/Brote: the authors did not translate the sequence for the signal peptide
A/Brote: the authors did not translate the sequence for the signal peptide
A/Brote: expression of opacity proteins is requiated by the number of translated repeat e)
of repeats place the start codon in frame with the rest of the protein
R/Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
EMBO J. 12, 641-650, 1993
A/Fitle: Variable opacity (Opa) outer membrane proteins account for the cell tropisms dis
A/Fitle: Variable opacity (Opa) outer membrane proteins account for the cell tropisms dis
A/Fitle: DAA
A/Rocession: 336328; MUD:93178439; PMID:8440254
A/Rocession: 24-260 cKUP>
A/Rocession: EMBL:Z18937; NID:949333; PIDN:CAA79370.1; PID:9940799
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A,Note: expression of opacity proteins is regulated by the number of translated repeat e1
of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       opacity protein opaJ precursor – Neisseria gonorrhoeae (strain MS11) (fragments)
N;Alternate names: outer membrane protein opa58
                                                                                                                                                                                                                                                                                               141 LGESAVYDFKLNDKFKPYIGARVAYGHVRHSIDSTKKTTEVTTILHGPGTTPTVYPGKNT 200
                                                                                                                                81 SVGYDFGGWRIAADYARYRKWNNNKYSVSIKELLRNKGNGNRTDLKAENQENGTFHAVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                    201 QNAHRESDSIRR--VGLGAVAGVGIDITPNLTLDAGYRYHYWGRLENTR-FKTHEASLGV
                                                                                                                                                                                                                                                                                                                                                                                            117 ----SDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reywords: cell surface component; transmembrane protein
11-10,11-23/Domain: signal sequence (fragments) #status predicted
42-260/Product: opacity protein opal #status predicted «MAT»
34-42/Domain: transmembrane #status predicted <TM1»
43-74/Domain: extracellular #status predicted <EXII»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 260;
                                                                                                                                                                                                                    83 IGASAIYDFDTQSPVKPYLGARLSLN--RASVD------LGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transmembrane #status predicted <TW4>
transmembrane #status predicted <TW5>
extracellular #status predicted <EXT3>
hypervariable region HV2
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#status predicted <EXT4>
#status predicted <TM8>
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;75-83/Domain: transmembrane #status predicted <TM2>
;88-94/Domain: transmembrane #status predicted <TM3>
;98-133/Domain: extracellular #status predicted <EXT2>
;101-128/Region: hypervariable region HV1
;134-148/Domain: transmembrane #status predicted <TM4>
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No. 3.9e-14;
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                                                SAGYRINDLRFAVDYTRYKNY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Neisseria gonorrhoeae
A; Variety: strain MS11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;212-224/Domain: transmembrane
F;228-254/Domain: transmembrane
F;337-251/Domain: extracellular
F;252-260/Domain: transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154-164/Domain: transmembrane
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Superfamily: opacity protein
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258 RYRF 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
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Nalternate names: outer membrane protein opak
Cispecies: Neisseria gonorrhoeae
A,Variety: strain MS11
C;Date: 13-Jan-1995 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
C;Date: 13-Jan-1995 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
C;Date: 13-Jan-1995 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
C;Date: 13-Jan-1995 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
C;Date: 13-Jan-1995 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
C;Date: 13-Jan-1995 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
C;Artile: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a family A,Rocession: S16610
A,Molecule type: DNA
A,Rocession: S16610
A,Molecule type: DNA
A,Rocession: S16610
A,Molecule type: DNA
A,Rocession S16610
A,Molecule type: DNA
A,Rocession of opacity proteins is regulated by the number of translated repeat e
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
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C;Superfamily: opacity protein
C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
F;1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
F;2-4261/Product: opacity protein opak #status predicted <MAT>
F;3-4-22/Domain: transmembrane #status predicted <TM1>
F;3-75/Domain: extracellular #status predicted <EXTI>
F;5-1-61/Region: semivariable region
F;76-84/Domain: transmembrane #status predicted <TM2>
F;89-95/Domain: transmembrane #status predicted <TM3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF
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                                                                                                                                                                                                                                                                                           Query Match 98.4%; Score 854; DB 2; Length 174; Best Local Similarity 98.3%; Pred. No. 1.1e-68; Matches 171; Conservative 0; Mismatches 3; Indels
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F;155-165/Domain: transmembrane #status predicted <TM5>
F;166-212/Domain: extracellular #status predicted <EXT3>
F;111-218/Region: hypervariable region HV2
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                                       A;Residues: 1-174 <PAR>
A;Cross-references: UNIPROT:P95372; GB:AL162754;
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: nspA; NMA0862
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Matches 73; Conservative
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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Matches 76; Conservative 27; Mismatches 67; Indels 88; Gaps 10;	
2 KKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFS- 47 	157 HPRVSVGYDFGGMRIAADYARYRKWNDNKYSVDIKELENKNUNKKDLKTENUEMGIFFAAV 81 YSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGG
48RRISAGYRINDLRFAVDYTRYKNYKAPSTDFK 79	
80LYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLG 115 	277 TÜNAHNQSNSIKKVGLGVIAGVGFDIIFALIDDIGIKINIMGKLENIK-FKINEASLGVK 172 VKP 174 :
116 GSDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVN 156	DD 336 YRF 338 RESULT 6
157 TVKNVRSGELSVGVRVKF 174 : :: : : 244 NTR-FKTHEASLGVRYRF 260	S16612 opacity protein opaE precursor - Neisseria gonorrhoeae (strain MS11) (fragments) C;Species: Neisseria gonorrhoeae A;Variety: atrain MS1 C:Date: 04-Jun-1997 #sequence revision 17-Oct-1997 #text change 17-Oct-1997
RESULT 5 S16613 opacity protein opaB precursor - Neisseria gonorrhoeae (strain MS11) (fragments) C;Species: Neisseria gonorrhoeae A;Variety: strain MS11 C;Date: 04-Jun-1997 #sequence revision 17-Oct-1997 #text change 17-Oct-1997	C. Accession: S16612 C.P. Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, I R.Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, I Mol. Microbiol. 5, 1889-1901, 1991 A. Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a famil A. Reference number: S16610; MUID:92114767; PMID:1815562 A. A. Accession: S16612 A. Molecule type: DNA
cession: S16613 at, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, M. Microbiol. 5, 1899-1901, 1991 the opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a family eference number: S16610; MUID:92114767; PMID:1815562	A, Residues: 1-258 <bha. 4.8="" a,="" authors="" by="" codon="" cross-references:="" did="" el="" embl.x52369="" experimental="" expression="" extoss-references:="" for="" frame="" in="" is="" m311,="" not="" note:="" number="" of="" opacity="" peptide="" place="" protein<="" proteins="" regulated="" repeat="" repeats="" rest="" sequence="" signal="" source:="" start="" strain="" td="" the="" translate="" translated="" variant="" w311,="" with=""></bha.>
tesidues: 1-338 cBHA> Irosa-references: EMBL.X52373 Xxperimental source: strain MSII, variant 4.8 Ote: the authors did not translate the sequence for the signal peptide lote: expression of opacity proteins is regulated by the number of translated repeat e repeats place the start codon in frame with the rest of the protein	A;Gene: opaE C;Superfamily: opacity protein C;Superfamily: coll surface component; transmembrane protein C;Keywords: cell surface component; transmembrane protein F;1-10,11-23/Domain: signal sequence (fragments) #status predicted <mat> F;24-258/Product: opacity protein opaE #status predicted <mmi> F;34-42/Domain: transmembrane #status predicted <mmi></mmi></mmi></mat>
nnetids: nne: opa8 nne: opa6 pperfamily: opacity protein sywords: cell surface component; transmembrane protein 13,14-104/Domain: signal sequence (fragments) #status predicted <8IG> 55-338/Product: opacity protein opa8 #status predicted <mat></mat>	F/50-60/Region: semivariable region F/50-60/Region: semivariable region F/75-83/Domain: transmembrane #status predicted <tm2> F/88-94/Domain: transmembrane #status predicted <tm3> F/88-94/Domain: extracellular #status predicted <ext2> F/101-125/Region: hypervariable region HV7</ext2></tm3></tm2>
F;124-155/Domain: extracellular #status predicted <ext1> F;124-14.[Region: semivariable region F;156-164/Domain: transmembrane #status predicted <tm2> F;166-175/Domain: transmembrane #status predicted <tm3> F;169-175/Domain: extracellular #status predicted <tm3> F;176-212/Domain: extracellular #status predicted <ext2> F;131-227/Domain: typervariable region My</ext2></tm3></tm3></tm2></ext1>	#status predicted #status predicted region HV2 #status predicted #status predicted #status predicted #status predicted
F;224-289/Domain: extracellular #status predicted <ext3> F;232-243/Domain: transmembrane #status predicted <tm>> F;232-243/Domain: transmembrane #status predicted <tm>> F;249-295/Region: hypervariable region HV2 F;290-302/Domain: transmembrane #status predicted <tm>> F;300-314/Domain: transmembrane #status predicted <tm>> F;315-329/Domain: extracellular #status predicted <ext4> F;310-338/Domain: transmembrane #status predicted <tm9></tm9></ext4></tm></tm></tm></tm></ext3>	27.8%; Best Local Similarity 29.7%; Matches 76; Conservative 2 KKALATLIALALPAAALA
Query Match 27.8%; Score 241.5; DB 2; Length 338; Best Local Similarity 30.0%; Pred. No. 5.8e-14; Matches 73; Conservative 25; Mismatches 66; Indels 79; Gaps 9; 10 ALALPAALAEG-ASGFYVQADAAHAKASSSLGSAKGF 46	6 KRESLLESSLLESSANGARGEDHGKGFIVÇALLATARENITHITEFFGIKKATSIVƏN 45GFSPRISAGYRINDLRFRAVDYTRYKNYKAPSTDFK
	OY 80LYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGG- 116

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opacity protein opa57 - Neisseria gonorrhoeae (strain MS11) (fragment)
N;Alternate names: outer membrane protein opa57
C;Species: Neisseria gonorrhoeae
A;Variety: strain MS11
C;Accession: S36343; S28626
R;Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
EMBO J. 12, 641-650, 1993
A;Rtle: Variable opacity (Opa) outer membrane proteins account for the cell tropisms dis A;Reference number: S36343; MJID:93178439; PMID:8440254
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A,Molecule type: DM.
A,Residues: 1-237 <KUP>
A,Residues: 1-237 <KUP>
A,Cross-references: UNIPROT:Q04880; EMBL:Z18935; NID:g49331; PIDN:CAA79368.1; PID:g94079;
A,Experimental source: strain MS11, variant P3
A,Note: expression of opacity proteins is regulated by the number of translated repeat el
of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 YKVLRTPGAHRESDSIRR--VGLGVIAGVGFDITPKLTLDAGYRYHNWGRLENTR-FKTH 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 HSIHPRVSVGYDFGGWRIAADYARYRKWSDNKYSVSIKNMRVHKHNSNRKWLKTENQENG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --FKLYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD--------LGG- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 -----SDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------ KNYKAPSTD-- 77
                                                                                                                                                                                                                                                                                                                                                                                                    14 SSLLFSSAAQAASEDGGRGPYVQADLAYAYEHITHDYPKPTDPSKGKISTVSDYFRNIRT 73
                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 237;
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:Keywords: cell surface component; transmembrane protein
;1-237/Product: opacity protein opa57 #status predicted <MAT>
;11-19/Domain: transmembrane #status predicted <TM1>
;20-51/Domain: extracellular. #status predicted <EXT1>
                                                                                                                                                                                                                                              64; Indels
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F;52-60/Domain: transmembrane #status predicted <TM2>
F;62-60/Domain: transmembrane #status predicted <TM3>
F;72-110/Domain: extracellular #status predicted <EXT2>
F;78-105/Region: hypervariable region HV1
F;111-125/Domain: transmembrane #status predicted <TM4>
F;131-141/Domain: transmembrane #status predicted <TM5>
F;142-188/Domain: extracellular #status predicted <EXT5>
F;147-194/Region: hypervariable region HV2
F;228-236/Domain: transmembrane #status predicted <TM7>
F;237-251/Domain: extracellular #status predicted <EXT4>
F;252-260/Domain: transmembrane #status predicted <TM8>
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F;205-213/Domain: transmembrane #status predicted <TW7>
F;214-228/Domain: extracellular #status predicted <EXTM2>
F;229-237/Domain: transmembrane #status predicted <TM8>
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29.6%; Pred. No. 4.7e-14;
iive 26; Mismatches 58
                                                                                                                                                          27.8%; Score 241; DB 1;
28.8%; Pred. No. 4.7e-14;
ive 30; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 ----PRISAGYRINDLRFAVDYTRY-----
                                                                                                                         Query Match
Best Local Similarity 28.0.
Best Local Conservative
72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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251 EASLGVRYRF 260
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les 71; Conserv
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Best Local S
Matches 71
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A) Note: the authors translated the codon CCA for residue 32 as Thr
A) Note: the authors did not translate the sequence for the signal peptide
A) Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
Cell 47, 61-71, 1986
A) Fittle: Opacity genes in Neisseria gonorrhoeae: control of phase and antigenic variatic A) Reference number: A90887; MUD:87002493; PMID:3093085
A) A) Reference number: A90887; MUD:87002493; PMID:3093085
A) M) Cocule type: DNA
A) Residues: 25-260
A) Note: this protein is synthesized as a precursor; however, the authors are uncertain a
                                                                                                                                                                                                                                                                                                                                                                                                                                     opacity protein opaC precursor - Neisseria gonorrhoeae (strain MSI1) (fragments)
NyAlternate names: opacity protein V0; triosephosphate dehydrogenase
C;Species: Neisseria gonorrhoeae
A;Variety etrain MSI1
C;Date: 31-Mar-1989 #sequence revision 17-Oct-1997 #text_change 09-Jul-2004
C;Accession: S16618; A24429; S36328; S28621
C;Accession: S16618; A24429; S36328; S28621
Mol. Microbiol. 5, 1889-1901, 1991
A;File: The opacity proteins of Neisseria gonorrhoeae strain MSI1 are encoded by a familal A;Reference number: S16610; MUID:92114767; PMID:1815562
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R;Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
BMEO J. 12, 641-650, 1993
A;Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms di
A;Reference number: S36328; MUID:93178439; PMID:8440254
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A; Residues: 25-260 < KUP>
A; Kleyer. T. F.
Rubmitted to the EMBL: 218927; NID: 949323; PIDN: CAA79360.1; PID: 9940789
R; Meyer. T. F.
Rubmitted to the EMBL Data Library, November 1992
A; Reference number: S28617
A; Accession: S28621
A; Molecule type: DNA
A; Residues: 25-260 < KNEY>
A; Accession: S28621
A; Molecule type: DNA
A; Residues: 25-260 < KNEY>
C; Genetics:
A; Cross references: EMBL: 218927; NID: 949323; PIDN: CAA79360.1; PID: 9340789
C; Genetics:
A; Gene: opaC
C; Superfamily: opacity protein
C; Superfamily: opacity protein
C; Superfamily: opacity protein
C; Superfamily: copacity protein
C; Superfamily: copacity protein
C; Superfamily: copacity protein opaC #status predicted < KMT>
F; 11, 12-24/Domain: signal sequence (fragments) #status predicted < KMT>
F; 55-43/Domain: transmembrane #status predicted < TM2>
F; 55-43/Domain: extracellular #status predicted < TM3>
F; 68-43/Domain: transmembrane #status predicted < TM3>
F; 68-44/Domain: transmembrane #status predicted < TM3>
F; 11-19/Pomain: extracellular #status predicted < TM4>
F; 11-10/Pomain: transmembrane #status predicted < TM4>
F; 11-10/Pomain: extracellular #status predicted < TM4>
F; 11-10/Pomain: transmembrane #status predicted < TM4>
F; 11-10/Pomain: transmembrane #status predicted < TM4>
F; 11-10/Pomain: transmembrane #status predicted < TM4>
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F; 11-10/Pomain: transmembrane #status predicted < TM4>
F; 11-10/Pomain: tr
        -----SDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTV 158
                                                      186 GTTPTVYPGKNTQDAHRESDSIRR--VGLGAVAGVGIDITPNLTLDAGYRYHYWGRLENT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: S16618
A;Molecule type: DNA
A;Residues: 1-260 eBHA>
A;Cross-references: UNIPROT:P11296; EMBL:X52370
                                                                                                                                                                                                                : :: | |:||| :|
244 R-FKTHEASLGVRYRF 258
                                                                                                                                                                       159 KNVRSGELSVGVRVKF 174
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A; Status: preliminary
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            117
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Db 126 NQENGTFHAVSSLGLSAVYDFKLNDKFKPYIGARVAYGHVRHSIDSTKKTTKFLTSSYGG 185 Qy 117SDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNV 161 Db 186 LNPTVYTBENTQNAHHQSNSIRRVGLGVIAGVGFDITPKLTLDTGYRYHYWGRLENTR-F 244 Qy 162 RSGELSVGVRVKF 174 ::	ch, fan, at e	F;43-74/Domair F;51-66/Regior F;51-66/Regior F;58-94/Domair F;95-139/Domair F;140-134/Regior F;140-134/Doma F;140-134/Doma F;160-170/Doma F;176-223/Regior F;218-232/Doma F;218-232/Doma F;243-227/Doma F;243-237/Doma F;243-257/Doma F;258-266/Doma F;258-266/Doma R;258-266/Doma R;258-266/Doma R;258-266/Doma	Db 6 KKPSLLPSSÅQÅAĠEDHGRĠPYĠĀDLĀYĀYEHITHDYPEQTAPKÄQLĞTVŠD 65 Qy 43AKGFSPRISAGYRINDLRFAVDYTRYK
ALAECASGEYVQADAAHA	ragments) 1997 tern, A.; encoded b and for ide ranslated	C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Seywords: cell surface component; transmembrane protein C;Seywords: cell surface component; transmembrane protein C;Seywords: cell surface component; transments) #status predicted F;24-257/Product: opacity protein opaF #status predicted <mit> F;24-257/Product: opacity protein opaF #status predicted <mit> F;34-42/Domain: transmembrane #status predicted <tmi> F;35-60/Region: semivariable region F;75-63/Domain: transmembrane #status predicted <tmi> F;88-94/Domain: transmembrane #status predicted <tmi> F;88-94/Domain: transmembrane #status predicted <tmi> F;101-126/Region: hypervariable region HV F;132-146/Domain: transmembrane #status predicted <tmi> F;162-162/Domain: transmembrane #status predicted <tmi> F;163-2108/Domain: transmembrane #status predicted <tmi> F;25-231/Domain: transmembrane #status predicted <tmi> F;234-248/Domain: transmembrane #status predicted <tmi> F;245-257/Domain: transmembrane #status predicted <tmi> F;245-257/Domain: transmembrane #status predicted <tmi< td=""><td>Query Match 27.7%; Score 240.5; DB 2; Length 257; Best Local Similarity 29.2%; Pred. No. 5.2e-14; Matches 74; Conservative 26; Mismatches 72; Indels 81; Gaps 9; QY 2 KKALATLIALALPAALAEGASGFYVQADAAHAKASSSLGSAK</td></tmi<></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></tmi></mit></mit>	Query Match 27.7%; Score 240.5; DB 2; Length 257; Best Local Similarity 29.2%; Pred. No. 5.2e-14; Matches 74; Conservative 26; Mismatches 72; Indels 81; Gaps 9; QY 2 KKALATLIALALPAALAEGASGFYVQADAAHAKASSSLGSAK

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A;Cross-references: UNIPROT:033388; EWBL:X63108
A;Experimental source: strain FAM18; clone pFLOB1700
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991
A;Note: only a part of the translation is shown
A;Note: expression of opacity proteins is regulated by the number of translated repeat el
                                                                                                                               82 SIGASAIYDFDTQSPVKPYLGARLSLN--RASVDL------GGSD----- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 PRVSVGYDFGDWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHAAS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Neisseria meningitidis
A;Variety: strain FAM18
C;Date: 04-Jun-1997 #sequence_revision 04-Jun-1997 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ajenie: Opposity protein
C; Superfamily: opacity protein
C; Keywords: cell surface component; transmembrane protein
C; Keywords: cell surface component; transmembrane prodicted
F; 1-19/Domain: stanal sequence (fragment) #status predicted «MI>
F; 20-254/Product: opacity protein opaB #status predicted «MI>
F; 31-39/Domain: transmembrane #status predicted «EXII>
F; 48-55/Region: semivariable region
F; 70-78/Domain: transmembrane #status predicted «IM2>
F; 81-89/Domain: transmembrane #status predicted «IM3>
F; 90-126/Domain: extracellular #status predicted «EXI2>
F; 90-126/Domain: extracellular #status predicted «EXI2>
F; 90-121/Region: hypervariable region HVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.3%; Score 237; DB 2; Length 254; 28.3%; Pred. No. 1e-13; ive 31; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;127-141/Domain: transmembrane #status predicted <TM4>F;127-141/Domain: transmembrane #status predicted <TM5>F;187-157/Domain: extracellular #status predicted <TM5>F;168-2105/Domain: extracellular #status predicted <EXT3>F;166-210/Domain: transmembrane #status predicted <TM6>F;223-230/Domain: transmembrane #status predicted <TM7>F;231-245/Domain: extracellular #status predicted <TM7>F;246-254/Domain: transmembrane #status gredicted <EXT4>F;246-254/Domain: transmembrane #status predicted <EXT4
N;Alternate names: outer membrane protein class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 PRISAGYRINDLRFAVDYTRYKNY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 27.33
Best Local Similarity 28.33
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-254 <AHO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 RVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RYHF 254
                                                                                                                                                                                                                                                                                                                                                         A; Accession: S20043
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                                                                                                                                                                                                                     subbly
spacity protein-related protein OPM1 precursor - Neisseria meningitidis (strain C1938) (
NyAlternate names: outer membrane protein class 5
C;Species Neisseria meningitidis
A;Variety: strain C1938
C;Date: 19-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
C;Date: 19-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
C;Date: 19-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
C;Date: 10-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
C;Date: 10-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
C;Date: 10-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
R;Stern, A.; Meyer, T.F.
Mol. Microbiol. 1, 5-12, 1987
A;Title: Common mechanism controlling phase and antigenic variation in pathogenic neise
A;Reference number: 808513; MUD:88260884; PMID:245511
A;Accession: 808514
A;Molecule type: DNA
A;Repaiduss: 1-258 «STES
A;Reperimental source: strain C1938
A;Robersimental source: strain C1938
A;Robersimental source: strain C1938
A;Robersimental source: strain frame with the rest of the protein
C;Genetics:
A;Gene: Opti
C;Genetics:
A;Gene: Opti
C;Keywords: Cell surface component; transmembrane protein OPM1 #status predicted *MAT>
F;1-13,14-21/Domain: stignal sequence (fragments) #status predicted *MAT>
F;22-258/Product: opacity protein-related protein OPM1 #status predicted *MAT>
F;22-258/Product: opacity protein-related protein OPM1 #status predicted *MAT>
F;34-41/Domain: transmembrane #status predicted *TM2>
F;34-29/Domain: transmembrane #status predicted *TM3>
F;34-29/Domain: transmembrane #status predicted *EMT2>
F;34-29/Domain: extracellular #status predicted *EMT2>
F;34-29/Domain: extracellular #status predicted *CM1>
F;34-29/Domain: extracellular #status predicted *CM2>
F;34-29/Domain: extracellular #status predicted *CM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    뽀
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820043
opacity protein B precursor (clone pFLOB1700) - Neisseria meningitidis (strain FAM18)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 -----DSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 TDPSKPPYHESHSISSLGLGVIAGVGFDITPKLTLDTGYRYHNWGRLENTR-FKTHEASL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 IHPRVSVGYDFGGWRIAADYASYRKWKESNFSTKKVTEEIKDNYKETKTEHQGNGSFHAT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 SSLGLSAIYDFKLNDKFKPYICARVAYGHVKHQVHSVETKTTTVTSKPKGGTPAGGPVIK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------KASSSLGS-----AKG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 FSPRISAGYRINDLRFAVDYTRYK------ 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;94-129/Domain: extracellular #status predicted <EXT2>
F;100-124/Region: hypervariable region HV1
F;130-144/Domain: transmembrane #status predicted <TM4>
F;150-160/Domain: transmembrane #status predicted <TM5>
F;161-209/Domain: extracellular #status predicted <EXT3>
F;166-215/Region: hypervariable region HV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;210-222/Domain: transmembrane #status predicted <TM6>F;226-234/Domain: transmembrane #status predicted <TM7>F;235-249/Domain: extracellular #status predicted <EXT4>F;250-258/Domain: transmembrane #status predicted <TM8>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 238; DB 2;
Pred. No. 8.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.4%; Scott No. c. 28.5%; Pred. No. c. ... 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 LIALALPAAALAEGASGFYVQADAAHA----
                |:: :: | |:||| :|
GRLENTR-FKTHEASLGVRYRF 266
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Best Local Similarity
Matches 70; Conserva
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GMRYRF
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opacity protein P.II precursor - Neisseria gonorrhoeae (strain F62-SF and others) (fragme C;Species: Neisseria gonorrhoeae A;Variety: strain F62-SF A;Variety: strain F62-SF C;Date: 30-Jun-1991 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004 C;Accession: S04380; S16504 R;Palmer, L.; Brooks, G.F.; Falkow, S.
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: :: | |:|:| :| 253 TR-FKTHEASLGMRYRF 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: S16360
A;Status: preliminary
A;Molecule type: protein
A;Residues: 24-34 <BAR>
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Best Local 9
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Matches
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Title: Expression of gonococcal protein II in Escherichia coli by translational fusion.
Reference number: S04380; MUID:89343653; PMID:2503682
                                                                                                                                     A;Cross-references: UNIPROT:Q50959; EMBL:X15780
A;Experimental source: strain F62-SF, serogroup IB-3; clone F62-SFG1
A;Note: the authors did not translate the sequence of the signal peptide
A;Note: expression of opacity proteins is regulated by the number of translated repeat
of repeats place the start codon in frame with the rest of the protein
K;Taha, M.K.; So, M.; Seifert, H.S.; Billyard, E.; Marchal, C.
EMBO J. 7, 4367-4378, 1988
A;Ttle: Pilin expression in Neisseria gonorrhoeae is under both positive and negative
A;Reference number: S02017; MUID:89210824; PMID:2854063
                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Status: translation not shown
A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 259-270 < 4TAH-
A, Cross-references: EMBL:X1396S
A, Experimental source: strain MS11A
A, Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
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DYFRNIRTHSVHPRVSVGYDFGGWRIAADYARYRKWNNNKYSVSIKELGRNDNSASGVRG 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------AKASSSLGSAK 44
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C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
E;1-10,11-23/Domain: signal sequence (fragments) #status predicted <8IG>
F;24-27/Droduct: opacity protein opaK #status predicted <MAT>
F;34-42/Domain: transmembrane #status predicted <TM1>
F;43-75/Domain: extracellular #status predicted <EXT1>
F;51-61/Region: semivariable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --NYKAPSTDFK-----LYSIGASALYDFDTQSPVKPYLGARLSL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 GF-----SPRISAGYRINDLRFAVDYTRYK-----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 237; DB 2; Length 270;
Pred. No. 1.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F/76-84/Domain: transmembrane #status predicted <TM2>
F/76-84/Domain: transmembrane #status predicted <TM3>
F/89-95/Domain: transmembrane #status predicted <EM3>
F/96-141/Domain: extracellular #status predicted <EM72>
F/102-136/Region: hypervariable region HV1
F/142-156/Domain: transmembrane #status predicted <TM4>
F/142-125/Domain: extracellular #status predicted <TM5>
F/173-221/Domain: extracellular #status predicted <EM75>
F/178-227/Region: hypervariable region HV2
F/222-224/Domain: transmembrane #status predicted <TM6>
F/238-246/Domain: transmembrane #status predicted <TM7>
F/247-261/Domain: extracellular #status predicted <TM7>
F/262-270/Domain: transmembrane #status predicted <TM7>
F/262-270/Domain: transmembrane #status predicted <TM7>
F/262-270/Domain: transmembrane #status predicted <TM7>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |: |: : : | |: | XHNWGRLENTR-FKTHEASLGVRYRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72; Conservative
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                                                      A;Accession: S04380
A;Molecule type: DNA
A;Residues: 1-270 <PAL>
                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: S16504
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NyAlternate names: outer membrane protein P.IIc
C;Species: Neisseria gonorrhoeae
A;Variety: strain JG3
A;Variety: strain JG3
C;Accession: S03095; S16360
R;Van der Ley, P. Mol. Microbiol. 2, 797-806, 1988
Mol. Microbiol. 2, 797-806, 1988
My:Title: Three copies of a single protein II-encoding sequence in the genome of Neisseria A;Reference number: S03095; MuID:89096501; PMID:3145386
                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-268 <VAN>
A;Cross-references: UNIPROT: P09888; EMBL:X12625
A;Cross-references: UNIPROT: P09888; EMBL:X12625
A;Experimental source: strain JG3
A;Dote: axpression of opacity proteins is regulated by the number of translated repeat el
A;Note: expression of opacity proteins is regulated by the protein
B;Barritt, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.
Infect. Immun. 55, 2026-2011, 1987
A;Ritle: Antigenic and structural differences among six proteins II expressed by a single
A;Reference number: S16360; MUID:87306843; PMID:3114142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 HSVHPRVSVGYDFGSWRIAADYARYRKWNNNKYSVSIKELLRNDNSASGVRGHLNIQTQK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 SNGGGKVSLSSKMPPKSAHHQSNSIRRVGLGVIAGVGFDITPNLTLDTGYRYHNWGRLEN 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 ---GGSDSFSQ-----TSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 ATLIALALPAAALAEGASGFYVQADAAHAKA-----SSSLGSAK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;220-232/Domain: transmembrane #status predicted <TM6>,236-244/Domain: transmembrane #status predicted <TM7>,345-259/Domain: extracellular #status predicted <EXTM5+,260-268/Domain: transmembrane #status predicted <TM8+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.2%; Score 236.5; DB 1
26.8%; Pred. No. 1.2e-13;
iive 32; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 -GFSPRISAGYRINDLRFAVDYTRYK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 VKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: opacity protein
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8

RESULT 15

KONH2C opacity protein P.IIc precursor - Neisseria gonorrhoeae (strain JS3) (fragments)

RESULT 14

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opacity protein opaH precursor - Neisseria gonorrhoeae (isolate 15063G)
N.Alternate names: cell invasion protein opaH
C.Species: Neisseria gonorrhoeae
A.Variety; isolate 15063G
C.Paccession: S7243
C.Accession: S7243
A.Title: The opaH locus of Neisseria gonorrhoeae MS11A is involved in epithelial cell in A.Title: The opaH locus of Neisseria gonorrhoeae MS11A is involved in epithelial cell in A.Paccession: S72343
A.Title: The opaH locus of Neisseria gonorrhoeae MS11A is involved in epithelial cell in A.Paccession: S72343
A.Accession: S72343
A.Accession: S72343
A.Accession: S72343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A) Residues: 1283 4WAL>
A) Residues: 1283 4WAL>
A) Residues: 1283 4WAL>
A) Cross-references: UNIPROT:Q50943; EWBL:U13708; NID:g535357; PIDN:AAA74082.1; PID:g5353
A) Experimental source: isolate 15063G
A) Experimental source: isolate 15063G
A) Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
A) Note: expression of opacity proteins is regulated by the number of translated repeat A; Note: expression of opacity protein is regulated by the number of translated repeat C; Superfamily: opacity protein
C; Keywords: cell surface component; transmembrane protein
C; Keywords: cell surface component; transmembrane protein
C; Keywords: cell surface component; transmembrane protein
C; Keywords: cell surface component; transmembrane prodicted <SIG>
F; 1487 Domain: signal sequence #status predicted <NAT>
F; 58-667 Domain: cransmembrane #status predicted <TMI>
F; 57-997 Domain: extracellular #status predicted <EXTI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 SLLSAAQAASEAMRGPYVQADLAFAAERITHDYPEPTGTKKGTISTVSDYFRNIRTHSVH 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;12-18/Domain: transmembrane #status predicted <TM2>
F;19-107/Domain: transmembrane #status predicted <TM3>
F;112-118/Domain: transmembrane #status predicted <TM3>
F;112-118/Domain: extracellular #status predicted <TM3>
F;112-15/Region: hypervariable region HV1
F;126-170/Domain: transmembrane #status predicted <TM4>
F;126-170/Domain: transmembrane #status predicted <TM4>
F;176-186/Domain: extracellular #status predicted <TM5>
F;182-240/Region: hypervariable region HV2
F;282-240/Region: hypervariable region GTM3>
F;282-240/Region: hypervariable region HV2
F;285-240/Region: transmembrane #status predicted <TM6>
F;285-287/Domain: transmembrane #status predicted <TM6>
F;286-274/Domain: extracellular #status predicted <TM8>
F;275-283/Domain: transmembrane #status predicted <TM8>
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Job time : 70 secs
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Best Local Similarity
Matches 68; Conserva
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280 RYRF 283
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                                                                                  ; Search time 357 Seconds
(without alignments)
249.585 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                        1 MKKALATLIALPAAALAE......VNTVKNVRSGELSVGVRVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1612378
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                 1612378 segs, 512079187 residues
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Q9K4T4
Q51126
Q51125
Q51125
Q9R3P5
OPRI NEIMC
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Maximum Match 100%
Listing first 45 summaries
                                                      protein search, using sw model
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P95372
Q7AR60
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Q65TE2
Q51124
Q9CM19
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Q9K4T9
Q9AE80
Q9R9A7
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Q7BW15
033388
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Q9RP18
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Q7DDM2
Q9RP17
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                                                                                    May 19, 2005, 20:24:55
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1: uniprot_sprot:*
2: uniprot_trembl:*
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MEDLINE=99386904; PubMed=1045695B;
REDLINE=99386904; PubMed=1045695B;
Cadieux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
"Bactericidal and cross-protective activities of a monoclonal antibody directed against Neisseria meningitidis NspA outer membrane protein.";
Infect. Immun. 67:4955-4959(1999).
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STRAIN=M986, NG6/88, and NGP165;

STRAIN=M986, NG6/88, and NGP165;

Moe Gr., Tan S., Granoff D.M.

Infected in Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains.";

LINFECT. Immun. 0:0-0(1999).

EMBL; US2066; AAD53283.1; --

R EMBL; AF175680; AAD53285.1; --

R EMBL; AF175681; AAD53286.1; --

R EMBL; AF175682; AAD53286.1; --

R EMBL; AF175689; PAD53286.1; --

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0015099; C:membrane; IEA.

R GO; GO:0015099; Prorin activity; IEA.

R InterPro; IPR003394; Porin_opacity.

R Signal.
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MEDLINE=97258610; PubMed=9104804;
Martin D., Cadieux N., Hamel J., Brodeur B.R.;
Highly conserved Nelsseria meningitidis surface protein confers protection against experimental infection.";
J. Exp. Med. 185:1173-1183(1997).
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Neisseriaceae; Neisseria.
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SEQUENCE FROM N.A.
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
00-JUL-2004 (TrEMBLrel. 27, Last annotation update)
00-deredLocusNames-NMB0663,
Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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99.5%; Score 864; DB 2;
Best Local Similarity 99.4%; Pred. No. 3.3e-69;
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TIGR; NMB0663; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0015288; F:porin activity; IEA.
InterPro; IPR003394; Porin_opacity.
Pfam; PF02462; Opacity; 1.
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61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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                                                                                                                                                                                                                                                                                                                                                          STRAIN=CU385;
Mod G.R., Tan S., Granoff D.M.;
"Differences in Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains.";
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"Differences in Surface Expression of Neisserial Surface Protein
among Neisseria meningitidis Group B strains.";
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                                                                                                                                                                                                   Neisseria meningitidis.
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
NCBI_TaxID=487;
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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EMBL, AF175678, AAD53281.1; -.

EMBL, AF175678, AAD53281.1; -.

EMBL, AF175678, AAD53281.1; -.

EMBL, AF175678, AAD53281.1; -.

EDB, 1P47, X-ray, A=20-174.

GO, GO:0015288, F:porin activity, IEA.

InterPro; IPR033394; Porin opacity.

EMM: PF02462; Opacity; 1.

ERQUENCE 174 AA; 18397 MW; E8B02767DDC6E109 CRC64;
                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Surface protein A.
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Pred. No. 3.3e-69;
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EMBL; AF175679; AAD53282.1; -.

EMBL; AF175677; AAD53280.1; -.

HSSP; OSPRPT7; 1F4T.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0015288; F:porin activity; IEA.
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Best Local Similarity 99.4
Matches 173; Conservative
PRELIMINARY;
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MEDLINE=9938604; PubMed=10456958;
MEDLINE=9938604; Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
Cadieux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
"Bactericidal and cross-protective activities of a monoclonal antibody
directed against Neisseria meningitidis NspA outer membrane protein.";
Infect. Immun. 67:4955-4959(1999).
EMBL, US2068; AAB41580.1; -.
PIR; B81932; B81932.
                                                                                                                            1 MKKALATLIALAIPAAALAEGASGFYVQADAAHAKASSSIGSAKGFSPRISAGYRINDLR
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-1997 (TrEMBLrel. 24, Last annotation update)
01-UNM-2003 (TrEMBLrel. 24, Last annotation update)
Outer membrane protein precursor.
Neisseria meningitidis.
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 98.4%; Score 854; DB 2; Length 174; Best Local Similarity 98.3%; Pred. No. 2.6e-68; Matches 171; Conservative 0; Mismatches 3; Indels
                                                      Length 174;
InterPro; IPR003394; Porin_opacity.
Pfam; PF02462; Opacity; 1.
SEQUENCE 174 AA; 18385 MW; ECF6F39A9286910E CRC64;
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                                                      Score 857; DB 2;
Pred. No. 1.4e-68;
1; Mismatches 2
                                                                                                                                                                                                                                                                                                                         174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, Q9RP17, 1P4T.
GO, GO:0016020; C:membrane; IEA.
GO, GO:0015288; F:porin activity; IEA.
InterPro; IPR003394; Porin_opacity.
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                                                      98.7%;
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Signal. 1 19
SIGNAL 19
                                                                                Matches 171; Conservative
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                                                      Query Match
Best Local Similarity
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PRELIMINARY;

Q7AR60 Q7AR60;

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61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN=22491 / Serogroup A / Serotype 4A;

MEDLINR=2029256; PubMed=10761919; DOI=10.1038/35006655;

MEDLINR=20222556; PubMed=10761919; DOI=10.1038/35006655;

Machill J., Achtman M., James K.D., Bentley S.D., Churcher C.M., Klee S.R., Morelli G., Bandem D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitchead S., Spratt B.G., Barrell B.G.;

"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
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STRAIN=NG3/88,

Moe G.R., Tan S., Granoff D.M.;

Moe G.R., Tan Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains.";

Infect. Immun. 0:0-0(1999).

Infect. Immun. 0:0-0(1999).

HSSP, QSPRD17; 1P4T.

GO; GO:0015020; C:membrane; IEA.

GO; GO:0015288; F:porin activity; IEA.

InterPro; IPR003394; Porin. opacity.

Pfam; PF02462; Opacity: 1.
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0
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
04. Juter membrane protein.
Name=nspA; OrderedLocusNames=NMA0862;
Neisseria meninglitidis (serogroup A).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
NCBL_TaxID=65699;
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Neisseriaceae; Neisseria.
NCBI_TaxID=487;
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98.3%; Pred. No. 2.6e-68;
ive 0; Mismatches 3; Indels
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Last annotation update)
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EMBL; AL162754; CAB84143.1; -.
GQ; GO:0016020; C:membrane; IEA.
GO; GO:0015288; E:porin activity; IEA.
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01-MAY-2000 (TrEMBLrel. 13, Created)
MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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Pfam; PF02462; Opacity; 1.
Complete proteome.
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Name=nspA;
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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GO; GO:0015288; F:porin activity; IEA.
InterPro; IPR003394; Porin opacity.
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GO; GO:0015289; F:porin activity; IEA.
InterPro; IPR003394; Porin_opacity.
Pfam; PF02462; Opacity; I.
                                                                              STRAIN=B2;
MEDLINE=99270944; PubMed=10338491;
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                                                                                                                                                      nfect. Immun. 67:2855-2861(1999)
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Best Local Similarity 94.3%;
Matches 164; Conservative
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                Neisseriaceae; Neisseria
NCBI_TaxID=485;
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                                                                                                                                                                                                                                                                                    Q9RP17; 1P4T.
                                                              SEQUENCE FROM N.A.
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                                                                                                           MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                           1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
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                                                               Gaps
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                                                                                                                                                                                                                                      121 SQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGMRVKF 174
                                                                                                                                                                                                                    121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moe G.R., Tan S., Granoff D.M.;
Moe G.R., Tan S., Granoff D.M.;

"Differences in Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains.";

Infect. Immun. 0:0-0(1999).

EMBL; AF175676; AAD53279.1; -.

EMBL; AF175676; CHMPAT.

GO; GO:0016020; CHMPATARE CHMPAT.

GO; GO:0015288; F:porin activity; IEA.

DIGGER DEGONORY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
Neisseriaceae, Neisseria.
NCBI_TaxID=487;
                                Length 174;
                                                              3; Indels
174 AA; 18355 MW; ECF6F38B9286800E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02462; Opacity; 1. S SEQUENCE 174 AA; 18357 MW; 0205AA1DA1B7F005 CRC64;
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P95343;
01-MAY-1997 (TrEMBLrel. 03, Created)
05-JUL-2004 (TrEMBLrel. 03, Last sequence update)
O6-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Outer membrane protein precursor (Surface protein A).
Neisseria gonorrhoeae.
                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                               Score 852; DB 2;
Pred. No. 3.9e-68;
                                                                                                                                                                                                                                                                                                                                174 AA
                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                Created)
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                               Query Match
Best Local Similarity 97.7%;
Matches 170; Conservative
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Best Local Similarity
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SEQUENCE
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RESULT 9 P95343 ID P953 AC 0953 DT 01-M DT 05-J DE Oute OS Neis

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61 FAVDYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDSF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-MCH 88;
MEDLINE-99386904; PubWed=10456958;
MEDLINE-99386904; PubWed=10456958;
Cadieux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
"Bactericidal and cross-protective activities of a monoclonal antibody
directed against Neisseria meningitidis NspA outer membrane protein.";
Infect. Immun. 67:4955-4959(1999).
EMBL; U52067; AAB41579.1;
HSSP; QSPRITY, IPAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
         Martin D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
Plante M., Cadieux N., Rioux C.R., Hamel J., Brodeur B.R., M. "Antigenic and molecular conservation of the gonococcal NspA protein.";
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Neisseria meningitidis.
Batteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriacaea; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Indels
                                                                                                                                                                                                                    Mingchun J.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 174 AA; 18337 MW; 1B558EC8A040841A CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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Pred. No. 1e-65;
2; Mismatches
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Pfam; PF02462; Opacity; 1.
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Best Local Similarity 35.1<sup>†</sup>
Matches 72; Conservative
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Best Local Similarity
Matches 69; Conserve
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                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                            STRAIN=MBEL55E;
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Q51124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 -GGSDSFSQT---SIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGV 170
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                                                                                                                                            1 MKKALAALIAILALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
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                                                                                                                                                                                                                                      61 FAVDYTRYKOYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSDS
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                                                                                                                  1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
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                                                                   Gaps
                                                                                                                                                                                                                                                                                                17; Gaps
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                                                                   1;
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Pasteurellaceae; Mannheimia.
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                     DB 2; Length 175;
                                                                 Indels
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SEQUENCE 177 Aa; 18969 MW; B6ACF0AA75915B57 CRC64;
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Last sequence update)
Last annotation update)
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
    Score 824.5; DB 2;
Pred. No. 1.1e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 35.0%; Score 303.5; DB 2 Local Similarity 40.2%; Pred. No. 3.8e-19; es 74; Conservative 25; Mismatches 68
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                                                                   0; Mismatches
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EMBL; AE016827; AAU38304.1; -.
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25-OCT-2004 (TrEMBLrel. 28, C.
25-OCT-2004 (TrEMBLrel. 28, L.
25-OCT-2004 (TrEMBLrel. 28, L.
Hypothetical protein.
ORFNames=MS1161;
                     95.0%;
                                                                   Matches 167; Conservative
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                                           Similarity
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                        Query Match
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Q65TE2
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A MEDLINE=9129089; PubMed=9467908;
A Hobbs M.M., Malorny B., Prasad P., Morelli G., Kusecek B.,
A Hobbs M.M., Malorny B., Prasad P., Morelli G., Kusecek B.,
A Hockels J.E., Cannon J.G., Achtman M.;
The Recombinational reassortment among open genes from ET-37 complex
Neisseria meningitidis isolates of diverse geographical origins.";
Microbiology 144:157-166(1998).
BEBL; U37255; AAC46101.1; -.
BEBL; U37255; AAC46101.1; -.
BERL; U37737; S7737.
BERL; DAPLT; LP4T.
BIR; ASP1, Q9R17; LP4T.
BIR; G0:0016228; F.porin activity; IEA.
BIR; CO:0016228; F.porin activity; IEA.
BIR; CO:00163394; Prorin opacity.
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Kim C.H., Jeong H., Hur C.-G., Kim J.G.;
Kim c.H., Jeong H., Hur C.-G., Kim J.G.;
Kim Jeepen Beater of the capnophilic rumen bacterium Mannheimia succipitorducens.";
Nat. Biotechnol. 0.0-0(2004).
Bhypothetical protein.
SEQUENCE 226 AA; 25460 MW; 106C558F9B4C1504 CRC64;
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Mannheimia succiniciproducens MBEL55E.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Mannheimia.
NCBL_TaxID=221988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis.
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 226;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.5%; Score 256; DB 2; Length 22
35.1%; Pred. No. 8.6e-15;
tive 26; Mismatches 67; Indels
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Ogacity outermembrane protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :: | | : | : | : | : | : | 1.0 IFDIENKGSNPFRSEKTTKLGYGFIAGAQYGLMTNLFVNGGIEYNRLGRPSDT-SVNQYG 177
                                                                                                                                                              74 PRVSVGYDFGGWRIAADYASYRKWKESNSSTKKVTEDIADNYKETKTEHQGNGSFHAASS 133
                                                                                                                                                                                                                             -----ASVDLGG----- 116
                                                                                                                                                                                                                                                          :| ||||||
134 LGLSAIYDFKLNDKFKPYIGARVAYGHVKHQVHSVETKTTTVTSKPTATSPQGGPIIQTD 193
                                                                                                                                                                                                                                                                                                                                    ----SDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKAVRSGELSVGV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 DLRFAVDYTRYKNYKAPS-----TDFKLYSIGASAIYDFDTQSPVKPYLGARLSLN 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 MKK---SLLVLAIGALCSLTASANFYVQGDLGVAKTKFSSYSEMNKTNIVPNVSVGYDLG 58
                                                                                                             82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. MKKALATLIALALPAAALAEGASGFYVQADAAHAK---ASSSLGSAKGFSPRISAGYRIN 57
  ----KASSSLGS-----AKGFS 47
                                                      14 LFSSÄAQAASEDSGHGPYYVQADLAYAAERITHDYPKATGANNTSTVSDYFRNIRAHSIH 73
                                                                                                             PRISAGYRINDLRFAVDYTRYK-----LYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21149866; PubMed=11248100; DOI=10.1073/pnas.051634598; May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.; "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. US. 98:3460-3465(2001).

EMBL; AE006143; AAK03109.1; -...
HSSP; QRPRIT; 1P4T.
GO; GO:0016220; C:membrane; IEA.
GO; GO:0015288; F:porin activity; IEA.
InterPro; IRR03394; Porin_opacity.
Ffam; PF02462; Opacity; 1.
Complete protecome.
SEQUENCE 186 AA; 20512 NW; IB17F0A4ACFC0157 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 28.4%; Score 246.5; DB 2; Length 186; Best Local Similarity, 32.3%; Pred. No. 4.9e-14; Matches 61; Conservative 32; Mismatches 77; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                          83 IGASAIYDFDTQSPVKPYLGARLSLNR-----
LIALALPAALAEGASGFYVQADAAHA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=opa; OrderedLocusNames=PM1025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 AKVGLRYDF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pasteurella multocida.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RYRF 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 RINDLRFAVDYTRYK----NYKAPSTDFK-----LYSIGASAI 88
                                                                                                                                                                                                                                                                                                                                                                                                    'Clonal descent and microevolution of Neisseria meningitidis during 30
                                                                                                                                                                                                                                                                                                          STRAIN=Z3524;
MEDLINE=98010345; PubMed=9350862;
Morelli G., Malorny B., Muller K., Seiler A., Wang J.F., del Valle J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 AALAEGA-SGFYVQADAAH-----AKASSSLGS-----AKGFSPRISAGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis.
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 28.1%; Score 244; DB 2; Length 23. Best Local Similarity 28.9%; Pred. No. 1.1e-13; Matches 67; Conservative 32; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 AA; 26134 MW; 005AD356E93BCC50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----ASVDLGG-
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Opacity protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP, Q9RP17; 1P4T.
GO, GO:0016020; C:membrane; IEA.
GO; GO:0015289; F:porin activity; IEA.
InterPro; IPR003394; Porin_opacity.
Pfam; PF02462; Opacity; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 YDFDTQSPVKPYLGARLSLNR----
                                                                                                                                                                                                                                                                                                                                                                                                                       years of epidemic spread.";
Mol. Microbiol. 25:1047-1064(1997)
EMBL; AF001195; AAC32716.1; -.
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        NCBI_TaxID=487;
                                                                                                                                                                                                                                                                                                                                                                              Achtman M.;
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completed: May 19, 2005, 21:01:04 ne : 359 secs

RESULT 15